

CC may be used diagnosing of treating diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
 CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
 CC Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 215 AA;

Query Match 100.0%; Score 1125; DB 3; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSBTEAVQGNPKLRICISCKREEVEATTVV 60
 DB 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSBTEAVQGNPKLRICISCKREEVEATTVV 60
 QY 61 EMFYRPEGCKPLIYERNGHQEVESPPQGRLONNGSKDLODVSTIVLNTLNDGSLYTC 120
 DB 61 EMFYRPEGCKPLIYERNGHQEVESPPQGRLONNGSKDLODVSTIVLNTLNDGSLYTC 120
 QY 121 NVSRFEFEARHPVKYTRRLPLRVTEBAGDFTSVSEIMMYILLVFLTLMLFTLMTYC 180
 DB 121 NVSRFEFEARHPVKYTRRLPLRVTEBAGDFTSVSEIMMYILLVFLTLMLFTLMTYC 180
 QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
 DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 2

AAB50243
 ID AAB50243 standard; protein; 215 AA.

AC AAB50243;
 XX 13-MAR-2001 (first entry)

DE Rat sodium channel beta3 protein A1rxa94h5.

KW Rat; sodium channel beta3 protein; A1rxa94h5; pain; sleep disorder;
 KM neurodegenerative disorder; mood disorder; muscle contraction.

OS Rattus sp.

PN W0200069912-A1.

XX 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US013144.

XX 14-MAY-1999; 99US-0134198P.

PA (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2001-122743/13.

DR N-PSDB; AAC90600.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 root ganglion cDNA library for use in chromosome mapping, forensic
 medicine, monitoring clinical trials and therapeutics.

XX Claim 9; Fig 2; 145PD; English.

CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated A1rxa94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics

SQ Sequence 215 AA;

Query Match 100.0%; Score 1125; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSBTEAVQGNPKLRICISCKREEVEATTVV 60
 DB 1 MPAFNRLLPLASLVLIYWRVCFVCEVPSBTEAVQGNPKLRICISCKREEVEATTVV 60
 QY 61 EMFYRPEGCKPLIYERNGHQEVESPPQGRLONNGSKDLODVSTIVLNTLNDGSLYTC 120
 DB 61 EMFYRPEGCKPLIYERNGHQEVESPPQGRLONNGSKDLODVSTIVLNTLNDGSLYTC 120
 QY 121 NVSRFEFEARHPVKYTRRLPLRVTEBAGDFTSVSEIMMYILLVFLTLMLFTLMTYC 180
 DB 121 NVSRFEFEARHPVKYTRRLPLRVTEBAGDFTSVSEIMMYILLVFLTLMLFTLMTYC 180
 QY 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
 DB 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 3

AAB3367
 ID AAB3367 standard; protein; 215 AA.

AC AAB3367;

XX 17-JUN-2003 (first entry)

DE Rat sodium channel beta-3 subunit.

KW Rat; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;
 KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;
 KM bipolar affective disorder; attention deficit disorder; phobic disorder;
 KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;
 KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;
 KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;
 KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;
 KM bone metabolism disorder; endometrial cell disorder; viral encephalitis;
 KM acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;
 KM poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;
 KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;
 KM pain.

OS Rattus norvegicus.

XX Key Location/Qualifiers

FT Domain 68..64

FT Domain /note= "Conserved motif"

FT Domain 104..122

XX EPI258495-A1.

PD 20-NOV-2002.

PF 09-MAY-2002; 2002EP-00253262.

XX 09-MAY-2001; 2001US-0289893P.

PA (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2003-185859/19.

PT New isolated human sodium channel beta-4 subunit nucleic acid molecule
 PT and polypeptide, useful for diagnosing and treating disorders with
 PT aberrant beta-4 subunit function or expression, such as neurological and
 PT cardiovascular diseases.

PS Disclosure; Page 56; 62pp; English.

XX
CC The invention relates to human sodium channel beta-4 subunit, 98359
CC polypeptides and polynucleotides. The methods and compositions of the
CC invention are useful for diagnosing, screening and treating disorders
CC associated with aberrant or deficient sodium channel beta-4 subunit
CC function or expression such as paroxysmal congenital, hyperkalaemic
CC periodic paralysis, epilepsy, psychomotoric diseases (anxiety or phobic
CC disorders, attention deficit disorder, obsessive-compulsive disorder and
CC bipolar affective disorder), dementia, cardiovascular disorders
CC (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),
CC neurological disorders (Alzheimer's or Parkinson's disease,
CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders
CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone
CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,
CC herpes simplex, poliomyelitis, viral encephalitis and peripheral
CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple
CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's
CC disease and Leigh disease). Polynucleotides of the invention are used to
CC identify an individual from a biological sample (tissue typing), and in
CC forensic identification of a biological sample. The invention is useful
CC in gene therapy. The present sequence is rat sodium channel beta-3
CC subunit. This sequence is used in the invention
CC
XX
SQ Sequence 215 AA:

Query Match 100.0%; Score 1125; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASIVLIYWRVCPVCVEVPSETEAVQGNPMKRCISCMKREVEATTVV 60
DB 1 MPAFNRLLPLASIVLIYWRVCPVCVEVPSETEAVQGNPMKRCISCMKREVEATTVV 60
QY 61 EMFYRPEGKDFLIYVRNGHVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120
DB 61 EMFYRPEGKDFLIYVRNGHVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120
QY 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDEFTSVSEIMYILVFLTLMLFIEMTYC 180
DB 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDEFTSVSEIMYILVFLTLMLFIEMTYC 180
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 4

AAB36002 standard; protein; 215 AA.

XX
AC AAB36002;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human beta3 subunit.
XX
XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;
XX cerebroprotective; vasotrophic; cardiant; nootropic; cycostatic;
XX dermatological; gene therapy; voltage-gated sodium channel; pain;
XX epilepsy; stroke; ischaemia; heart disease; Jacobson Syndrome;
XX familial nonchromaffin paraganglioma; phenylketonuria;
XX Charcot Marie Tooth disease.
XX
OS Homo sapiens.
XX
PN MO200063367-A1.
XX
PD 26-OCT-2000.
XX
PF 24-FEB-2000; 2000WO-EP001783.
XX
PR 15-APR-1999; 99US-0129473P.

XX
PA (WARR) WARNER LAMBERT CO.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Cox P, Dixon A, Jackson A, Morgan K;
XX
DR WPI; 2000-665241/64.
XX
DR N-PSDB; AAC67837.
XX

PS Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
XX stroke.
XX
XX Claim 34; Fig 4; 88pp; English.

XX
XX The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobson Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
CC
XX
SQ Sequence 215 AA:

Query Match 98.2%; Score 1105; DB 3; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.4e-97;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFNRLLPLASIVLIYWRVCPVCVEVPSETEAVQGNPMKRCISCMKREVEATTVV 60
DB 1 MPAFNRLLPLASIVLIYWRVCPVCVEVPSETEAVQGNPMKRCISCMKREVEATTVV 60
QY 61 EMFYRPEGKDFLIYVRNGHVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120
DB 61 EMFYRPEGKDFLIYVRNGHVESPPQGRLOMNSKDLQDVSTIVLNTLNDGLTYC 120
QY 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDEFTSVSEIMYILVFLTLMLFIEMTYC 180
DB 121 NVSRREFEFHRRFPVKTTRILPLRVTEAGEDEFTSVSEIMYILVFLTLMLFIEMTYC 180
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 5

AAB85206 standard; protein; 215 AA.

XX
AC AAB85206;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human novel sodium channel beta1-like subunit.
XX
XX Sodium channel; sensory neurone specific channel; beta1-like subunit;
XX SNS; therapeutic; pain; analgesic.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 38..122
FT Domain /note="immunoglobulin domain"
FT Domain 157..176
FT Domain /note="transmembrane domain"
XX
PN MO200144293-A2.

PD 21-JUN-2001.
XX
XX 14-DEC-2000; 2000MO-GB004802.
XX
XX 17-DEC-1999; 99GB-00029970.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Plumbton M, Powell AJ, Saneau P;
XX
XX WPI: 2001-398129/42.
XX
XX N-PSDB; AAF84146.
XX
XX Novel sub-unit for voltage-gated sodium channel proteins for producing
XX agents useful for treating pain.
XX
XX Claim 1; Fig 2; 31pp; English.
XX
XX The invention provides a novel beta1-like sub-unit for voltage-gated
XX sodium ion channel polypeptide, specifically a sensory neurone specific
XX channel (SNS) subunit. The novel beta1-like subunit is useful for
XX producing a therapeutic agent which is useful treating pain in a patient.
XX The subunit can be expressed by standard recombinant methodology. The
XX present sequence represents a human novel sodium channel beta1-like
XX subunit
XX
XX Sequence 215 AA;
XX
XX

Query Match 98.2%; Score 1105; DB 4; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.4e-97;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAPRLPLPLASLVLIYWRVCFPCVEVPSETEAVQGNPKLRICISCMKREEVEATTIV 60
DB 1 MPAPRLPLPLASLVLIYWRVCFPCVEVPSETEAVQGNPKLRICISCMKREEVEATTIV 60
QY 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120
DB 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120
QY 121 NVSRREFEFAHRRPFVKTRRLPLRVTEEAGEFTSVSEIMWYILLVFLTMLIEMTYC 180
DB 121 NVSRREFEFAHRRPFVKTRRLPLRVTEEAGEFTSVSEIMWYILLVFLTMLIEMTYC 180
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 6
ABB05689
ID ABB05689 standard; protein; 215 AA.
XX
XX ABB05689;
XX

DT 30-APR-2002 (first entry)
XX
XX Human signal transduction protein clone amy2_2f18.
XX
XX Human, foetal brain; foetal kidney; melanoma; testis; amygdala;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX WO200198454-A2.
XX
XX 27-DEC-2001.
XX
XX 25-APR-2001; 2001WO-IB002050.
XX
XX 25-APR-2000; 2000US-0199380P.
XX
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
XX

XX
XX Wiemann S;
XX
XX WPI: 2002-055860/07.
XX
XX N-PSDB; ABA93727.
XX
XX Human cDNA sequences and clones derived from human fetal brain, fetal
XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
XX screening and therapy.
XX
XX Claim 1; Page 176; 611pp; English.
XX
XX

CC The present invention describes assemblages and computer readable media
CC comprising novel human cDNA sequences and clones derived from human
CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
CC present invention which encode the proteins given in ABB05662 to
CC ABB05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in a variety of applications, for example
CC they may be used in profiling assays, for providing large arrays of human
CC genetic material for implementing large-scale screening strategies and
CC for treating diseases via gene therapy procedures
XX
XX Sequence 215 AA;
XX

Query Match 98.2%; Score 1105; DB 5; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.4e-97;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAPRLPLPLASLVLIYWRVCFPCVEVPSETEAVQGNPKLRICISCMKREEVEATTIV 60
DB 1 MPAPRLPLPLASLVLIYWRVCFPCVEVPSETEAVQGNPKLRICISCMKREEVEATTIV 60
QY 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120
DB 61 EMFYRPEGKDFLIYERNQHOEVESPFQGRLOMNGSKDLDVSIITVAVNTLNDGLTYC 120
QY 121 NVSRREFEFAHRRPFVKTRRLPLRVTEEAGEFTSVSEIMWYILLVFLTMLIEMTYC 180
DB 121 NVSRREFEFAHRRPFVKTRRLPLRVTEEAGEFTSVSEIMWYILLVFLTMLIEMTYC 180
QY 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215
DB 181 YRKVSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 7
AAE35366
ID AAE35366 standard; protein; 215 AA.
XX
XX AAE35366;
XX

DT 17-JUN-2003 (first entry)
XX
XX Human sodium channel beta-3 subunit.
XX
XX Human; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;
XX shock; hypertension; psychiatric disease; obsessive-compulsive disorder;
XX bipolar affective disorder; attention deficit disorder; phobic disorder;
XX cardiovascular disorder; neurological disorder; spinocerebellar ataxia;
XX Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;
XX autoimmune disorder; cellular proliferative disorder; Krabbe's disease;
XX metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;
XX bone metabolism disorder; endothelial cell disorder; viral encephalitis;
XX acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;
XX poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;
XX dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;
XX pain.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 38..70
XX
XX

FT /note= "Conserved motif"
FT Domain 104, .122
FT /note= "Conserved motif"
XX EPI258495-A1.
XX
XX
XX 20-NOV-2002.
XX
XX 09-MAY-2002; 2002EP-00253262.
XX
XX 09-MAY-2001; 2001US-0289893P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI; 2003-185859/19.
XX
XX New isolated human sodium channel beta-4 subunit nucleic acid molecule
XX and polypeptide, useful for diagnosing and treating disorders with
XX aberrant beta-4 subunit function or expression, such as neurological and
XX cardiovascular diseases.
XX
XX Disclosure; Page 55-56; 62pp; English.
XX
XX The invention relates to human sodium channel beta-4 subunit, 98359
XX polypeptides and polynucleotides. The methods and compositions of the
XX invention are useful for diagnosing, screening and treating disorders
XX associated with aberrant or deficient sodium channel beta-4 subunit
XX function or expression such as paroxysmal congenital, hyperkalemic
XX periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic
XX disorders, attention deficit disorder, obsessive-compulsive disorder and
XX bipolar affective disorder), dementia, cardiovascular disorders
XX (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),
XX neurological disorders (Alzheimer's or Parkinson's disease,
XX spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders
XX (diabetes, arthritis), cellular proliferative disorders (cancer), bone
XX metabolism disorders, liver disorders, viral infections (AIDS, rabies,
XX herpes simplex, poliomyelitis, viral encephalitis and peripheral
XX neuropathy), endothelial cell disorders, demyelinating diseases (multiple
XX sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's
XX disease and Leigh disease). Polynucleotides of the invention are used to
XX identify an individual from a biological sample (tissue typing), and in
XX forensic identification of a biological sample. The invention is useful
XX in gene therapy. The present sequence is human sodium channel beta-3
XX subunit. This sequence is used in the invention
XX
SQ Sequence 215 AA;
Query Match 98.2%; Score 1105; DB 6; Length 215;
Best Local Similarity 98.1%; Pred. No. 1,4e-97;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPAFNLLPLASIVLIVYVCPVCEVSETEAVQGNPMKLRCSCKMREBEVATTYV 60
DB 1 MPAFNLLPLASIVLIVYVCPVCEVSETEAVQGNPMKLRCSCKMREBEVATTYV 60
QY 61 EWFYRPEGKDFLIYERNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120
DB 61 EWFYRPEGKDFLIYERNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120
QY 121 NVSRREFEFHARFPVKTTRILIPRTVEAGDEPTSVSSIMYIILVFLTMLLIEMTYC 180
DB 121 NVSRREFEFHARFPVKTTRILIPRTVEAGDEPTSVSSIMYIILVFLTMLLIEMTYC 180
QY 181 YRKVSRAEBAQENASDYLAIPSENKENSVPVPEE 215
DB 181 YRKVSRAEBAQENASDYLAIPSENKENSVPVPEE 215
RESULT 8
ABR83183
ID ABR83183 standard; protein; 215 AA.

XX
XX ABR83183;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human SCN3B protein.
XX
XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
XX neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiant;
XX hypotensive; gene therapy; SCN3B; human.
XX
XX Homo sapiens.
XX
XX W02003072751-A2.
XX
XX 04-SEP-2003.
XX
XX 25-FEB-2003; 2003WO-US006010.
XX
XX 25-FEB-2002; 2002US-0359382P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX George AL, Lossin C;
XX
XX WPI; 2003-712725/67.
XX
XX N-PDB; ACF57870.
XX
XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
XX screening for modulators, for treating e.g. epilepsy.
XX
XX Disclosure; Page 145-147; 176pp; English.
XX
XX The invention relates to a recombinantly expressed and isolated human
XX SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
XX incorporated into a cell, is used to screen for specific modulators,
XX potentially useful as anticonvulsant, antiepileptic, neuroprotective,
XX analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
XX epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
XX motor endplate diseases, hypertension, congestive heart failure and
XX muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
XX and metastatic cancer cell lines). These activities can also be provided
XX by gene therapy vectors that express (I) or the modulators. The
XX modulators, also antibodies directed against (I), are used to detect
XX sodium channel polypeptides. The present sequence represents a human
XX SCN3B protein
XX
SQ Sequence 215 AA;
Query Match 98.2%; Score 1105; DB 7; Length 215;
Best Local Similarity 98.1%; Pred. No. 1,4e-97;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPAFNLLPLASIVLIVYVCPVCEVSETEAVQGNPMKLRCSCKMREBEVATTYV 60
DB 1 MPAFNLLPLASIVLIVYVCPVCEVSETEAVQGNPMKLRCSCKMREBEVATTYV 60
QY 61 EWFYRPEGKDFLIYERNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120
DB 61 EWFYRPEGKDFLIYERNGHGVESPPQGRLOMNGSKDLQDVSTIVLVNTLNDGSLYTC 120
QY 121 NVSRREFEFHARFPVKTTRILIPRTVEAGDEPTSVSSIMYIILVFLTMLLIEMTYC 180
DB 121 NVSRREFEFHARFPVKTTRILIPRTVEAGDEPTSVSSIMYIILVFLTMLLIEMTYC 180
QY 181 YRKVSRAEBAQENASDYLAIPSENKENSVPVPEE 215
DB 181 YRKVSRAEBAQENASDYLAIPSENKENSVPVPEE 215
RESULT 9
AAM79212
ID AAM79212 standard; protein; 195 AA.

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XX AA0792212;
AC 06-NOV-2001 (first entry)
DT
DE Human protein SEQ ID NO 1874.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-0064936.
XX
XX 15-SEP-2000; 2000US-00653561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HSE-) HSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK52345.
XX
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 4260; 6221pp; English.
XX
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
XX
XX Sequence 195 AA;
XX
XX Query Match 89.7%; Score 1009; DB 4; Length 195;
XX Best Local Similarity 98.5%; Pred. No. 2e-88;
XX Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 121 NVSRFEFEARHPVKTRLLPLRVTEAGEDFTSVSEIMYILLVFLTLMLFIEMTYC 180
OY 181 YRKVSKAEAAQENA 195
DB 181 YRKVSKAEAAQENA 195
XX
XX RESULT 10
XX AAB50245
XX ID AAB50245 standard; protein; 191 AA.
XX
XX AAB50245;
XX
XX 13-MAR-2001 (first entry)
XX
XX Rat sodium channel beta3 protein A1rx94h5 mature protein.
XX
XX Rat; sodium channel beta3 protein; A1rx94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction.
XX
XX Rattus sp.
XX
XX WO200069912-A1.
XX
XX 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013144.
XX
XX 14-MAY-1999; 99US-0134198P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI; 2001-122743/13.
XX
XX N-PSDB; AAC90600.
XX
XX
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
XX root ganglion cDNA library for use in chromosome mapping, forensic
XX medicine, monitoring clinical trials and therapeutics.
XX
XX Claim 9; Fig 2; 145pp; English.
XX
XX
XX The present invention provides the protein and coding sequences of the
XX rat sodium channel beta3 protein, designated A1rx94h5. This protein is
XX involved in the generation of pain and other sensory or perceptive nerve
XX impulses, in the establishment and endurance of mood, neurodegenerative
XX and sleep disorders, and in the control of muscle contraction, including
XX movements such as the heartbeat, digestion and vascular tone. The
XX sequences can be used in predictive medicine, screening and diagnostic
XX assays, and in pharmacogenomics
XX
XX Sequence 191 AA;
XX
XX Query Match 88.5%; Score 996; DB 4; Length 191;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-87;
XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

ABG22577 standard; protein; 369 AA.

AC ABG22577;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22568.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

PI MPI; 2001-639362/73.

DR N-PSDB; AAS6764.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 52936; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The CC diagnostic, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic CC amino acid sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 369 AA;

Query Match 82.4%; Score 927.5; DB 4; Length 369;

Best Local Similarity 92.3%; Pred. No. 2.8e-80;

Matches 181; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 1 MPANFLPLASLVLYWVRCFVCEVPSSETEAVQGNPMKLRCTSCMKREVEATTYV 59
DB 127 MPANFLPLASLVLYWVRCFVCEVPSSETEAVQGNPMKLRCTSCMKREVEATTYV 186
QY 60 VEMFYRPEGKDLIYEYRNGHQEVESPFQGRLOMNGSKDLOVSTIVNTLNDGLVT 119

DB 187 VEMFYRPEGKDLIYEYRNGHQEVESPFQGRLOMNGSKDLOVSTIVNTLNDGLVT 246

QY 120 CNVSREFEERARPPFKYTRLLPLRTEBAGDFTSVSEIMMYILLVLTMLFLEMITY 179

DB 247 CNVSREFEERARPPFKYTRLLPLRTEBAGDFTSVSEIMMYILLVLTMLFLEMITY 306

QY 180 CYRKVSKAEBAQENA 195

DB 307 CYRKVSKAEBAQENA 322

RESULT 12

AAB36021 standard; protein; 159 AA.

AC AAB36021;

DT 15-FEB-2001 (first entry)

DE Rat beta3 subunit peptide, SEQ ID NO: 23.

KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;

KW vasotropic; cardiac; nocotropic; cytostatic; dermatological;

KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;

KW ischaemia; heart disease; Jacobsen Syndrome;

KW familial nonchromaffin paraganglioma; phenylketonuria;

KW Charcot Marie Tooth disease.

OS Rattus sp.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI MPI; 2000-665241/64.

Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

PS Claim 36; Page 76-77; 88pp; English.

The present sequence is given in the claims of a specification relating CC to a novel family of beta sub-unit proteins from a voltage-gated sodium CC channel. Human and rat beta sub-units, which have been collectively CC identified as beta3, have been isolated. The polynucleotides and CC polypeptides are useful for screening for agonists and antagonists of CC sodium channels. The agonists, antagonists, proteins and nucleic acids CC may be used diagnosing of treating diseases or conditions associated with CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia, CC heart disease, Jacobsen Syndrome, familial Nonchromaffin Paraganglioma, CC phenylketonuria and Charcot Marie Tooth disease

SQ Sequence 159 AA;

Query Match 74.8%; Score 842; DB 3; Length 159;

Best Local Similarity 100.0%; Pred. No. 1.6e-72;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANFLPLASLVLYWVRCFVCEVPSSETEAVQGNPMKLRCTSCMKREVEATTYV 60
DB 1 MPANFLPLASLVLYWVRCFVCEVPSSETEAVQGNPMKLRCTSCMKREVEATTYV 60

Db 121 NVSREFFEAHRPVRTTLRLPLRVTEAGEDEFTSVV 157

RESULT 15

ABG22576
ID ABG22576 standard; protein; 1176 AA.

XX ABG22576;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22567.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX MO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS86763.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20, SEQ ID NO 52935; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1176 AA;

Query Match 61.2%; Score 689; DB 4; Length 1176;

Best Local Similarity 99.2%; Pred. No. 8.8e-57;

Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 VRVCFPVCEVPSSETEAQGNPMKLRICISCMKREVEATTVEWFPYRGGKDFLIYEYR 78
DB 987 VSVCFPVCEVPSSETEAQGNPMKLRICISCMKREVEATTVEWFPYRGGKDFLIYEYR 1046

QY 79 NGHQEVESPFQGRLOMNGSKDLODVSTVLTANTLNDGLTYTCNVSRFEFFEAHRPFVKTT 138

Db 1047 NGHQEVESPFQGRLOMNGSKDLODVSTVLTANTLNDGLTYTCNVSRFEFFEAHRPFVKTT 1106

QY 139 RLPLRVTEE 148

Db 1107 RLPLRVTEE 1116

Search completed: March 31, 2005, 20:17:51
Job time : 128.5 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:11:14 ; Search time 30 Seconds
(without alignments)
534.985 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125
Sequence: 1 MPANRLPLASLVILYWR.....SDYLAIPEKNSKNSVYVPE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------------------|-------------------|
| 1 | 466.5 | 41.5 | 204 | 4 | US-09-949-016-8240 | Sequence 8240, Ap |
| 2 | 147.5 | 13.1 | 215 | 4 | US-09-949-016-6658 | Sequence 6658, Ap |
| 3 | 147.5 | 13.1 | 263 | 4 | US-09-949-016-10819 | Sequence 10819, A |
| 4 | 131 | 11.6 | 269 | 3 | US-09-430-503-2 | Sequence 2, Appl |
| 5 | 131 | 11.6 | 269 | 3 | US-09-430-503-4 | Sequence 4, Appl |
| 6 | 131 | 11.6 | 269 | 3 | US-09-430-503-6 | Sequence 6, Appl |
| 7 | 131 | 11.6 | 269 | 3 | US-09-430-503-8 | Sequence 8, Appl |
| 8 | 131 | 11.6 | 313 | 4 | US-09-949-016-10974 | Sequence 10974, A |
| 9 | 126.5 | 11.2 | 270 | 3 | US-09-430-503-26 | Sequence 26, Appl |
| 10 | 126.5 | 11.2 | 270 | 3 | US-09-430-503-30 | Sequence 30, Appl |
| 11 | 125 | 11.1 | 199 | 3 | US-09-430-503-44 | Sequence 44, Appl |
| 12 | 125 | 11.1 | 199 | 3 | US-09-430-503-48 | Sequence 48, Appl |
| 13 | 125 | 11.1 | 270 | 3 | US-09-430-503-32 | Sequence 32, Appl |
| 14 | 125 | 11.1 | 270 | 3 | US-09-430-503-42 | Sequence 42, Appl |
| 15 | 123 | 10.9 | 199 | 3 | US-09-430-503-46 | Sequence 46, Appl |
| 16 | 123 | 10.9 | 199 | 3 | US-09-430-503-18 | Sequence 18, Appl |
| 17 | 123 | 10.9 | 209 | 3 | US-09-430-503-20 | Sequence 20, Appl |
| 18 | 123 | 10.9 | 209 | 3 | US-09-430-503-22 | Sequence 22, Appl |
| 19 | 123 | 10.9 | 209 | 3 | US-09-430-503-24 | Sequence 24, Appl |
| 20 | 118 | 10.5 | 159 | 3 | US-09-430-503-34 | Sequence 34, Appl |
| 21 | 118 | 10.5 | 159 | 3 | US-09-430-503-36 | Sequence 36, Appl |
| 22 | 118 | 10.5 | 159 | 3 | US-09-430-503-38 | Sequence 38, Appl |
| 23 | 118 | 10.5 | 159 | 3 | US-09-430-503-40 | Sequence 40, Appl |
| 24 | 106.5 | 9.5 | 318 | 4 | US-09-656-952-2 | Sequence 2, Appl |
| 25 | 106.5 | 9.5 | 215 | 4 | US-09-949-016-6523 | Sequence 6523, Ap |
| 26 | 106 | 9.4 | 225 | 4 | US-09-949-016-10820 | Sequence 10820, A |
| 27 | 106 | 9.4 | 225 | 4 | US-09-949-016-10820 | Sequence 10820, A |

| | | | | | | |
|----|------|-----|-----|---|-------------------|-------------------|
| 28 | 105 | 9.3 | 519 | 3 | US-08-996-338-21 | Sequence 21, Appl |
| 29 | 105 | 9.3 | 519 | 4 | US-09-556-972-21 | Sequence 21, Appl |
| 30 | 105 | 9.3 | 537 | 1 | US-08-604-333-4 | Sequence 4, Appl |
| 31 | 105 | 9.3 | 537 | 3 | US-09-110-618-4 | Sequence 4, Appl |
| 32 | 105 | 9.3 | 537 | 3 | US-09-173-151A-29 | Sequence 29, Appl |
| 33 | 105 | 9.3 | 537 | 4 | US-09-578-178-4 | Sequence 4, Appl |
| 34 | 105 | 9.3 | 537 | 4 | US-09-577-806-4 | Sequence 4, Appl |
| 35 | 105 | 9.3 | 537 | 4 | US-09-621-502-8 | Sequence 8, Appl |
| 36 | 105 | 9.3 | 801 | 3 | US-09-383-630-6 | Sequence 6, Appl |
| 37 | 103 | 9.2 | 344 | 4 | US-09-656-952-19 | Sequence 19, Appl |
| 38 | 103 | 9.2 | 394 | 4 | US-09-656-952-20 | Sequence 20, Appl |
| 39 | 103 | 9.2 | 394 | 4 | US-09-855-323-17 | Sequence 17, Appl |
| 40 | 98.5 | 8.8 | 316 | 4 | US-09-397-243D-13 | Sequence 13, Appl |
| 41 | 98.5 | 8.8 | 408 | 3 | US-09-724-864-62 | Sequence 62, Appl |
| 42 | 97.5 | 8.7 | 131 | 1 | US-08-129-930B-95 | Sequence 95, Appl |
| 43 | 97.5 | 8.7 | 131 | 3 | US-08-134-346A-50 | Sequence 50, Appl |
| 44 | 97.5 | 8.7 | 131 | 3 | US-08-976-288A-95 | Sequence 95, Appl |
| 45 | 97 | 8.6 | 541 | 1 | US-08-604-333-2 | Sequence 2, Appl |

ALIGNMENTS

```
RESULT 1
US-09-949-016-8240
; Sequence 8240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0010307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8240
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8240

Query Match      41.5%; Score 466.5; DB 4; Length 204;
Best Local Similarity 51.6%; Pred. No. 2.8e-42;
Matches 98; Conservative 28; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPSEETAVOQNPMLKRCISCMKREVEATTVWVFYRPEGKDFL- IYERYNGHOEV 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 CVEVDSETEAVVGMFTKXICISCKRSEETNAETFEWTRQKGTETFEVILRYENEVLDL 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 85 EEP-FOGRLQNGS---KDLQDVSTIVANVTIANDSGLYTCNVSRFEFEARHPFKTR 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 EEDERPEGVVWNGSGRTDLDLSIFITNVVYHSGDDECHYRLLFFENEHNTSVYK 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 140 LPLPLRTEAGEDEFTSVSEIMMYILVFLTLMFLFEMITCYRKAVSKA-EAQAQNASDY 198
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 KHIIEVDKANDRMASIVSEIMTYLIVLITLVAVEMITCYKIAAETTAQENASEY 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 199 LAIPSENKEN 208
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 LAITSEKSEN 196

RESULT 2
US-09-949-016-6658
; Sequence 6658, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6658
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6658

Query Match 13.1%; Score 147.5; DB 4; Length 215;
Best Local Similarity 27.9%; Pred. No. 8,5e-08;
Matches 55; Conservative 27; Mismatches 72; Indels 43; Gaps 8;

QY 7 LPLASLVLIYVWVCFPVCEVPSETEAVQGNPKMKRCISCMKREVEATTVEMFYRP 66
DB 21 LMP1AA-VEIYTSRV-----LEAVNGTDARLKTCTSSFPAPVDALTVT-WNFRP 67
QY 67 -EGG-KDFLIYERNHGOEVESPPQGRLOWNSKDLQDVSTVLTNLTNSGLTYCNVSR 124
DB 68 LDGGEQGFVYHYHIDPFQPMGSRFKDRVSDGNPERDASILLMKLQDPDDNGTYCQYKN 127
QY 125 EEFEEAHRPVPKTRLLPLRVTEAGEDFTSV-----SEIMYLLV-----FLTLM 173
DB 128 -----PPDVGVIGELIRLSVHTVRSEIHLFLALIGSACALMIITVI 170
QY 174 FIEMTYCRKYSKAEBA 190
DB 171 VVVLFGHYRKKRWAEBA 187

RESULT 3
US-09-949-016-10819
; Sequence 10819, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10819
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10819

Query Match 13.1%; Score 147.5; DB 4; Length 263;
Best Local Similarity 27.9%; Pred. No. 1.1e-07;
Matches 55; Conservative 27; Mismatches 72; Indels 43; Gaps 8;

QY 7 LPLASLVLIYVWVCFPVCEVPSETEAVQGNPKMKRCISCMKREVEATTVEMFYRP 66
DB 7 LPLASLVLIYVWVCFPVCEVPSETEAVQGNPKMKRCISCMKREVEATTVEMFYRP 66

DB 69 LMP1AA-VEIYTSRV-----LEAVNGTDARLKTCTSSFPAPVDALTVT-WNFRP 115
QY 67 -EGG-KDFLIYERNHGOEVESPPQGRLOWNSKDLQDVSTVLTNLTNSGLTYCNVSR 124
DB 116 LDGGEQGFVYHYHIDPFQPMGSRFKDRVSDGNPERDASILLMKLQDPDDNGTYCQYKN 175
QY 125 EEFEEAHRPVPKTRLLPLRVTEAGEDFTSV-----SEIMYLLV-----FLTLM 173
DB 176 -----PPDVGVIGELIRLSVHTVRSEIHLFLALIGSACALMIITVI 218
QY 174 FIEMTYCRKYSKAEBA 190
DB 219 VVVLFGHYRKKRWAEBA 235

RESULT 4
US-09-430-503-2
; Sequence 2, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-2

Query Match 11.6%; Score 131; DB 3; Length 269;
Best Local Similarity 23.0%; Pred. No. 7.1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSETEAVQGNPKMKRCISCMKREVEAT---TVEMFYRPGGKDFL-IYERNHQ 82
DB 40 VYTPKEIRIVANGTQGLTC---KFKSTTGGTGSVMSFPQEGADTVTFPHYSQGV 95
QY 83 EVES--PPQGRLOWNSKDLQDVSTVLTNLTNSGLTYCNVSRFEFEAHRPVPKTRRL 140
DB 96 YLGVPFQKRIISVAGDLDKDKDASINIMQGFHNGTYICVKN----- 139
QY 141 IPLRVTEAGEDFTSVSE-----IMYLLVFLTLMFIEMTYC--YRK----- 183
DB 140 -PPDIVQPGIRIRLYVEKENLPVFPVWVVGIVAVVLGLTLISMLAVLYRKKNSKR 198
QY 184 -----VSKAEAAQENASD---YLAIPESENKENVV 211
DB 199 DYTGCSTSESISPVKQAPRKSPDTEGLVKSIPSGSHQGPVI 240

RESULT 5
US-09-430-503-4
; Sequence 4, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-4

Query Match 11.6%; Score 131; DB 3; Length 269;
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPMKLRICISCKREVEAT---TVWEPYRPGGKDFL-IEYRNHQ 82
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVSPFHYSGQV 95
 QY 83 EVES--PFGRLQWNSKDLQDVSTVAVNTLNDGSLYTGNVSRFEFEHRRPVKTRRL 140
 DB 96 YLGNYPFPKDRISWAGDLDDKASININEMQFIHNGTYICDVKN-----139
 QY 141 IPLRVTEAGEDPTSVSE-----IMMYILVFLTLMFIEMYIC--YRK-----183
 DB 140 -PPDIVQPGHRLIYVEKENLVPFPVWVVGIVTAVVLGLTLISMTLAVLYRRKNSKR 198
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENSUV 211
 DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLSGSHQGPVI 240

RESULT 6
 US-09-430-503-6
 ; Sequence 6, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:

APPLICANT: Zhao, Zhizhuang
 TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 CURRENT FILING DATE: 1999-10-29
 NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-6

Query Match 11.6%; Score 131; DB 3; Length 269;
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPMKLRICISCKREVEAT---TVWEPYRPGGKDFL-IEYRNHQ 82
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVSPFHYSGQV 95
 QY 83 EVES--PFGRLQWNSKDLQDVSTVAVNTLNDGSLYTGNVSRFEFEHRRPVKTRRL 140
 DB 96 YLGNYPFPKDRISWAGDLDDKASININEMQFIHNGTYICDVKN-----139
 QY 141 IPLRVTEAGEDPTSVSE-----IMMYILVFLTLMFIEMYIC--YRK-----183
 DB 140 -PPDIVQPGHRLIYVEKENLVPFPVWVVGIVTAVVLGLTLISMTLAVLYRRKNSKR 198
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENSUV 211
 DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLSGSHQGPVI 240

RESULT 7
 US-09-430-503-8
 ; Sequence 8, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 APPLICANT: Zhao, Zhizhuang
 TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-8

Query Match 11.6%; Score 131; DB 3; Length 269;
 Best Local Similarity 23.0%; Pred. No. 7.1e-06;
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPMKLRICISCKREVEAT---TVWEPYRPGGKDFL-IEYRNHQ 82
 DB 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVSPFHYSGQV 95
 QY 83 EVES--PFGRLQWNSKDLQDVSTVAVNTLNDGSLYTGNVSRFEFEHRRPVKTRRL 140
 DB 96 YLGNYPFPKDRISWAGDLDDKASININEMQFIHNGTYICDVKN-----139
 QY 141 IPLRVTEAGEDPTSVSE-----IMMYILVFLTLMFIEMYIC--YRK-----183
 DB 140 -PPDIVQPGHRLIYVEKENLVPFPVWVVGIVTAVVLGLTLISMTLAVLYRRKNSKR 198
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENSUV 211
 DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLSGSHQGPVI 240

RESULT 8
 US-09-949-016-10974
 ; Sequence 10974, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT FILING DATE: 2000-04-14
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10974
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-10974

Query Match 11.6%; Score 131; DB 4; Length 313;
 Best Local Similarity 23.0%; Pred. No. 8.8e-06;
 Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPSSEAVQGNPMKLRICISCKREVEAT---TVWEPYRPGGKDFL-IEYRNHQ 82
 DB 84 VYTPKEIFVANGTQGLTCTC---KFKSTSTTGLTSVMSFQEGADTVSPFHYSGQV 139
 QY 83 EVES--PFGRLQWNSKDLQDVSTVAVNTLNDGSLYTGNVSRFEFEHRRPVKTRRL 140
 DB 140 YLGNYPFPKDRISWAGDLDDKASININEMQFIHNGTYICDVKN-----183
 QY 141 IPLRVTEAGEDPTSVSE-----IMMYILVFLTLMFIEMYIC--YRK-----183
 DB 184 -PPDIVQPGHRLIYVEKENLVPFPVWVVGIVTAVVLGLTLISMTLAVLYRRKNSKR 242
 QY 184 -----VSKAEBAQENASD---YLAIPSENKENSUV 211
 DB 243 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLSGSHQGPVI 284

RESULT 9
US-09-430-503-26
; Sequence 26, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-430-503-26

Query Match 11.2%; Score 126.5; DB 3; Length 270;
Best Local Similarity 26.9%; Pred. No. 2.2e-05;
Matches 54; Conservative 29; Mismatches 89; Indels 29; Gaps 10;

QY 2 PAFNRL--PLASLVLIYWRVCPVCEVSETEAVOGNPMKRLCISCMKREVEAT-- 57
DB 14 PARRRWLMSVLAAMGLTARIS-ALVHTPKEIFVANGTQKLTCTF----DSPNTTGW 68
QY 58 -TVWEMFYRPGGKDFL-IYEYRNGHOVES--PFGRLQWNGSKDLDVSTIVANTLN 113
DB 69 LTTVWSFQPDGTDGSAVFFHYSQGVYIGDYPFKDRTVWAGDLDKDKDASININIQAV 128
QY 114 DSGLYTCVNSREFEFEARHP-----FKTTRLILPRTVEAGDFTSVSEIMMYILLV 167
DB 129 HNGTYICVKNPDDIV-RPGHRLHVEIDNLVFLWVVVG-TVTAVVGLTLLISLV 186
QY 168 FLTLMFLFEMITCYRKVSKE 188
DB 187 LVLY-----RRKSKRD 199

RESULT 10
US-09-430-503-30
; Sequence 30, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-430-503-30

Query Match 11.2%; Score 126.5; DB 3; Length 270;
Best Local Similarity 26.9%; Pred. No. 2.2e-05;
Matches 54; Conservative 29; Mismatches 89; Indels 29; Gaps 10;

QY 2 PAFNRL--PLASLVLIYWRVCPVCEVSETEAVOGNPMKRLCISCMKREVEAT-- 57
DB 14 PARRRWLMSVLAAMGLTARIS-ALVHTPKEIFVANGTQKLTCTF----DSPNTTGW 68
QY 58 -TVWEMFYRPGGKDFL-IYEYRNGHOVES--PFGRLQWNGSKDLDVSTIVANTLN 113
DB 69 LTTVWSFQPDGTDGSAVFFHYSQGVYIGDYPFKDRTVWAGDLDKDKDASININIQAV 128

QY 114 DSGLYTCVNSREFEFEARHP-----FKTTRLILPRTVEAGDFTSVSEIMMYILLV 167
DB 129 HNGTYICVKNPDDIV-RPGHRLHVEIDNLVFLWVVVG-TVTAVVGLTLLISLV 186
QY 168 FLTLMFLFEMITCYRKVSKE 188
DB 187 LVLY-----RRKSKRD 199

RESULT 11
US-09-430-503-44
; Sequence 44, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-44

Query Match 11.1%; Score 125; DB 3; Length 199;
Best Local Similarity 25.4%; Pred. No. 2e-05;
Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVSSETEAVOGNPMKRLCISCMKREVEAT--TVWEMFYRPGGKDFL-IYEYRNGHQ 82
DB 40 VYTPKEIVFVANGTQKLTCTF-----KFKSTTGGTISVMSFGPBGADTVTSFFHYSQGV 95
QY 83 EVES--PFGRLQWNGSKDLDVSTIVANTLNDSGLYTCVNSREFEFEARHPVYKTRL 140
DB 96 YIGNYPPFKDRISWAGDLDKDKDASININEMQFIHNGTYICVKN----- 139
QY 141 IPLRTVEAGDFTSVSE-----IMMYILLVFLTLMFLFEMITCY--RKVSKE 187
DB 140 -PPDIVQPGHRLRYVEKENLPVFPVWVVVGIVAVVGLTLLISLAVLYRKSKR 198
QY 188 E 188
DB 199 D 199

RESULT 12
US-09-430-503-48
; Sequence 48, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-48

Query Match 11.1%; Score 125; DB 3; Length 199;
Best Local Similarity 25.4%; Pred. No. 2e-05;
Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVSSETEAVOGNPMKRLCISCMKREVEAT--TVWEMFYRPGGKDFL-IYEYRNGHQ 82

Db 40 VYTPKEIFVANGTQGLTCTF---KFKSTSTTGLTSVSNFQEGADTTVSFPHYSOGQV 95
 QY 83 EVES--PFGRLQWNGSKDLOVSIIVLAVTLNDSGLYTCNVSREPEFAHRPFVKTTRL 140
 Db 96 YIGNYPFQDRISWAGDLKDKASINIEIMQFIHNGTYICVKN-----F 139
 QY 141 IPLRTEAGEDFTSVSE-----IMMYILLVFLTLMFIEMICY---RKVSKA 187
 Db 140 -PEDIYVQGHIRLYVEKENLFPVFWVVGIVTAVVLGLTLLISMLAVLYRRKSKR 198
 QY 188 E 188
 Db 199 D 199

RESULT 13
 US-09-430-503-28
 ; Sequence 28, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 28
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-430-503-28

Query Match 11.1%; Score 125; DB 3; Length 270;
 Best Local Similarity 27.0%; Pred. No. 3.2e-05;
 Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;

QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT---TYVEMFYRPEGKDFL-IYERNHGO 82
 Db 40 VHTPKEIFVANGTQGLTCTF---DSPNTGMLTIVSWSFQPDGDSAVSFPHYSOGQV 95
 QY 83 EVES--PFGRLQWNGSKDLOVSIIVLAVTLNDSGLYTCNVSREPEFAHRPFVKTTRL 140
 Db 96 YIGDYPPFQDRISWAGDLKDKASINIEIMQFIHNGTYICVKNPPDIYV-RGHIRLHV 154
 QY 135 VKTTRLIPLRTEAGEDFTSVSEIMMYILLVFLTLMFIEMICYRKVSKAE 188
 Db 155 VEIDNLVFLVWVVG-TVTAVVLGLTLLISLVLVLY-----RRKSKRD 199

RESULT 14
 US-09-430-503-32
 ; Sequence 32, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 32
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-430-503-32

Query Match 11.1%; Score 125; DB 3; Length 270;
 Best Local Similarity 27.0%; Pred. No. 3.2e-05;

Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;
 QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT---TYVEMFYRPEGKDFL-IYERNHGO 82
 Db 40 VHTPKEIFVANGTQGLTCTF---DSPNTGMLTIVSWSFQPDGDSAVSFPHYSOGQV 95
 QY 83 EVES--PFGRLQWNGSKDLOVSIIVLAVTLNDSGLYTCNVSREPEFAHRPFVKTTRL 140
 Db 96 YIGDYPPFQDRISWAGDLKDKASINIEIMQFIHNGTYICVKNPPDIYV-RGHIRLHV 154
 QY 135 VKTTRLIPLRTEAGEDFTSVSEIMMYILLVFLTLMFIEMICYRKVSKAE 188
 Db 155 VEIDNLVFLVWVVG-TVTAVVLGLTLLISLVLVLY-----RRKSKRD 199

RESULT 15
 US-09-430-503-42
 ; Sequence 42, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 42
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-42

Query Match 10.9%; Score 123; DB 3; Length 199;
 Best Local Similarity 25.4%; Pred. No. 3.4e-05;
 Matches 46; Conservative 21; Mismatches 74; Indels 40; Gaps 7;

QY 27 VEVPSTEAQGNPMKLRICISCKREVEAT---TYVEMFYRPEGKDFL-IYERNHGO 82
 Db 40 VHTPKEIFVANGTQGLTCTF---KFKSTSTTGLTSVSNFQEGADTTVSFPHYSOGQV 95
 QY 83 EVES--PFGRLQWNGSKDLOVSIIVLAVTLNDSGLYTCNVSREPEFAHRPFVKTTRL 140
 Db 96 YIGNYPFQDRISWAGDLKDKASINIEIMQFIHNGTYICVKN-----F 139
 QY 141 IPLRTEAGEDFTSVSE-----IMMYILLVFLTLMFIEMICY---RKVSKA 187
 Db 140 -PEDIYVQGHIRLYVEKENLFPVFWVVGIVTAVVLGLTLLISMLAVLYRRKSKR 198
 QY 188 E 188
 Db 199 D 199

Search completed: March 31, 2005, 20:23:54
 Job time : 32 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 20:21:59 ; Search time 91.5 Seconds
(without alignments)
779.153 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125
Sequence: 1 MPAFRLPLASIVLITWVR.....SDYLAIPISENKSNVYVBE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
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10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1125 | 100.0 | 215 | 11 | US-09-977-579-1 |
| 2 | 1125 | 100.0 | 215 | 13 | US-10-029-191-2 |
| 3 | 1125 | 100.0 | 215 | 14 | US-10-142-201B-12 |
| 4 | 1105 | 98.2 | 215 | 11 | US-09-977-579-2 |
| 5 | 1105 | 98.2 | 215 | 14 | US-10-142-201B-11 |
| 6 | 996 | 88.5 | 191 | 13 | US-10-029-191-4 |
| 7 | 842 | 74.8 | 159 | 11 | US-09-977-579-23 |
| 8 | 832 | 74.0 | 159 | 11 | US-09-977-579-22 |
| 9 | 597 | 53.1 | 111 | 13 | US-10-029-191-5 |
| 10 | 470.5 | 41.8 | 218 | 13 | US-10-029-191-20 |
| 11 | 466.5 | 41.5 | 218 | 14 | US-10-142-201B-8 |
| 12 | 466.5 | 41.5 | 218 | 16 | US-10-477-272-2 |
| 13 | 463.5 | 41.2 | 218 | 11 | US-09-977-579-44 |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 14 | 292 | 26.0 | 58 | 13 | US-10-029-191-7 | Sequence 7, Appl |
| 15 | 257.5 | 22.9 | 268 | 9 | US-09-875-456A-14 | Sequence 14, Appl |
| 16 | 257.5 | 22.9 | 268 | 15 | US-10-401-916-14 | Sequence 14, Appl |
| 17 | 230 | 20.4 | 74 | 15 | US-10-276-774-2068 | Sequence 2068, Ap |
| 18 | 206 | 18.3 | 39 | 11 | US-09-977-579-18 | Sequence 18, Appl |
| 19 | 196 | 17.4 | 39 | 11 | US-09-977-579-17 | Sequence 17, Appl |
| 20 | 165 | 14.7 | 34 | 11 | US-09-977-579-47 | Sequence 47, Appl |
| 21 | 164 | 14.6 | 248 | 15 | US-10-016-248-54 | Sequence 54, Appl |
| 22 | 164 | 14.6 | 251 | 15 | US-10-016-248-52 | Sequence 52, Appl |
| 23 | 164 | 14.6 | 258 | 15 | US-10-016-248-53 | Sequence 53, Appl |
| 24 | 162 | 14.4 | 219 | 15 | US-10-016-248-51 | Sequence 51, Appl |
| 25 | 161 | 14.3 | 34 | 11 | US-09-977-579-31 | Sequence 31, Appl |
| 26 | 160 | 14.2 | 248 | 15 | US-10-205-331-110 | Sequence 110, App |
| 27 | 153 | 13.6 | 248 | 14 | US-10-273-601-1 | Sequence 12, Appl |
| 28 | 152 | 13.5 | 235 | 13 | US-10-053-107-12 | Sequence 12, Appl |
| 29 | 152 | 13.5 | 235 | 14 | US-10-227-884-238 | Sequence 238, App |
| 30 | 152 | 13.5 | 235 | 14 | US-10-230-163-238 | Sequence 238, App |
| 31 | 152 | 13.5 | 235 | 14 | US-10-230-338-238 | Sequence 238, App |
| 32 | 152 | 13.5 | 235 | 14 | US-10-218-631-238 | Sequence 238, App |
| 33 | 152 | 13.5 | 235 | 14 | US-10-230-414-238 | Sequence 238, App |
| 34 | 152 | 13.5 | 235 | 14 | US-10-213-145-12 | Sequence 12, Appl |
| 35 | 152 | 13.5 | 235 | 14 | US-10-232-224-238 | Sequence 238, App |
| 36 | 152 | 13.5 | 235 | 14 | US-10-216-159A-238 | Sequence 238, App |
| 37 | 152 | 13.5 | 235 | 14 | US-10-218-849-238 | Sequence 238, App |
| 38 | 152 | 13.5 | 235 | 14 | US-10-227-873-238 | Sequence 238, App |
| 39 | 152 | 13.5 | 235 | 14 | US-10-227-883-238 | Sequence 238, App |
| 40 | 152 | 13.5 | 235 | 14 | US-10-219-076-238 | Sequence 238, App |
| 41 | 152 | 13.5 | 235 | 14 | US-10-230-434-238 | Sequence 238, App |
| 42 | 152 | 13.5 | 235 | 14 | US-10-213-199-12 | Sequence 12, Appl |
| 43 | 152 | 13.5 | 235 | 14 | US-10-219-003-238 | Sequence 238, App |
| 44 | 152 | 13.5 | 235 | 14 | US-10-219-075-238 | Sequence 238, App |
| 45 | 152 | 13.5 | 235 | 14 | US-10-219-464-238 | Sequence 238, App |

ALIGNMENTS

RESULT 1
US-09-977-579-1
; Sequence 1, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Rat
US-09-977-579-1

Query Match 100.0%; Score 1125; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.8e-105; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAFRLPLASIVLITWVRCPVCEVPSSETEAVQGNPMKURCTISCKMRBEVEATTVV 60
DB 1 MPAFRLPLASIVLITWVRCPVCEVPSSETEAVQGNPMKURCTISCKMRBEVEATTVV 60
QY 61 EMFYREGGKDFLIYRYRNGHGVESPPQGRLOMNGSKLODVSTIVLNTLNDGLYTC 120
DB 61 EMFYREGGKDFLIYRYRNGHGVESPPQGRLOMNGSKLODVSTIVLNTLNDGLYTC 120

Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 2

US-10-029-191-2
; Sequence 2, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00X/5U1
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-2

Query Match 100.0%; Score 1125; DB 13; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.8e-105;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Db 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Qy 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Db 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 3

US-10-142-201B-12
; Sequence 12, Application US/10142201B
; Publication No. US20030022205A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP12001-106PLN(M)
; CURRENT FILING DATE: 2002-05-09
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-10-142-201B-12

Query Match 100.0%; Score 1125; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.8e-105;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Db 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Qy 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Db 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 4

US-09-977-579-2
; Sequence 2, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-579-2

Query Match 98.2%; Score 1105; DB 11; Length 215;
Best Local Similarity 98.1%; Pred. No. 3e-103;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Db 1 MPANRLPLASLVLIYWRVCFVCEVPSSTEAQGNPKMLRCISCMKREVEATTIV 60
Qy 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Db 61 EMFYRPEGKDFLIYEYNGHQEVESPPQGRLOMNGSKDLOVSTIVNTLVNLSGLTYC 120
Qy 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Db 121 NVSRFEFEARHPVKTTRLPLRVTEBAGEDFTSVSEIMMYILLVFLTLMFIEMTYC 180
Qy 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215
Db 181 YRKVSKAEBAQAENASDYLAIPSENKENSVPVVEE 215

RESULT 5

US-10-142-201B-11
; Sequence 11, Application US/10142201B
; Publication No. US20030022205A1
; GENERAL INFORMATION:

```

; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP12001-1061RN(M)
; CURRENT APPLICATION NUMBER: US/10/142, 201B
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/269, 893
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-201B-11

Query Match          98.2%; Score 1105; DB 14; Length 215;
Best Local Similarity 98.1%; Pred. No. 3e-103;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVQGNPMKLRCSCKRREEVEATTVV 60
DB 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVQGNPMKLRCSCKRREEVEATTVV 60
QY 61 EMFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSITVANTLNDGSLYTC 120
DB 61 EMFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSITVANTLNDGSLYTC 120
QY 121 NVSRFEFEFAHRPFVKTTRLIPLRVTEBAGEDFTSVSEIMMYLLVFLTMLFIEMITC 180
DB 121 NVSRFEFEFAHRPFVKTTRLIPLRVTEBAGEDFTSVSEIMMYLLVFLTMLFIEMITC 180
QY 181 YRKYSKAEBAQENASDYLAIPSENKENSVPVEE 215
DB 181 YRKYSKAEBAQENASDYLAIPSENKENSVPVEE 215

RESULT 6
US-10-029-191-4
; Sequence 4, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029, 191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569, 978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134, 198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-4

Query Match          88.5%; Score 996; DB 13; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.6e-92;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCVEVSETEAVQGNPMKLRCSCKRREEVEATTVVEMFYRPGGKDFLIYVRNGHVE 84
DB 1 VCVEVSETEAVQGNPMKLRCSCKRREEVEATTVVEMFYRPGGKDFLIYVRNGHVE 84
QY 85 ESPFOGRLOMNSKDLQDVSITVANTLNDGSLYTCVNSRFEFEFAHRPFVKTTRLIPLR 144
DB 61 ESPFOGRLOMNSKDLQDVSITVANTLNDGSLYTCVNSRFEFEFAHRPFVKTTRLIPLR 120
```

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QY 145 VTEBAGEDFTSVSEIMMYLLVFLTMLFIEMITCYRKYSKAEBAQENASDYLAIPSE 204
DB 121 VTEBAGEDFTSVSEIMMYLLVFLTMLFIEMITCYRKYSKAEBAQENASDYLAIPSE 180
QY 205 NKENSVPVEE 215
DB 181 NKENSVPVEE 191

RESULT 7
US-09-977-579-23
; Sequence 23, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129, 473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Rat
US-09-977-579-23

Query Match          74.8%; Score 842; DB 11; Length 159;
Best Local Similarity 100.0%; Pred. No. 7.4e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVQGNPMKLRCSCKRREEVEATTVV 60
DB 1 MPANRLPLASVLIYWRVCPVCEVPSSETEAVQGNPMKLRCSCKRREEVEATTVV 60
QY 61 EMFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSITVANTLNDGSLYTC 120
DB 61 EMFYRPGGKDFLIYVRNGHVESPFQGRLOMNSKDLQDVSITVANTLNDGSLYTC 120
QY 121 NVSRFEFEFAHRPFVKTTRLIPLRVTEBAGEDFTSVSE 159
DB 121 NVSRFEFEFAHRPFVKTTRLIPLRVTEBAGEDFTSVSE 159

RESULT 8
US-09-977-579-22
; Sequence 22, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129, 473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-579-22
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Query Match 74.0%; Score 832; DB 11; Length 159;
Best Local Similarity 98.7%; Pred. No. 7.6e-76;
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIIYWRVCPVCEVPSSETEAQGNPMKLRICSCMKREVEATTVV 60
DB 1 MPAFRLPLASLVIIYWRVCPVCEVPSSETEAQGNPMKLRICSCMKREVEATTVV 60
QY 61 EMPYRPEGKDFLIYEYRNGHOEVSPQGRLOMNGSKDLOVSTIVNTLNDGLTYC 120
DB 61 EMPYRPEGKDFLIYEYRNGHOEVSPQGRLOMNGSKDLOVSTIVNTLNDGLTYC 120
QY 121 NVSRFEFEAHRPFVKTTRLPLRYTEAGDEFTSVSE 159
DB 121 NVSRFEFEAHRPFVKTTRLPLRYTEAGDEFTSVSE 159

RESULT 9

US-10-029-191-5
; Sequence 5, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:

; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/501
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-5

Query Match 53.1%; Score 597; DB 13; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.6e-52;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCVEVPSSETEAQGNPMKLRICSCMKREVEATTVVEMFYRPEGKDFLIYEYRNGHOEV 84
DB 1 VCVEVPSSETEAQGNPMKLRICSCMKREVEATTVVEMFYRPEGKDFLIYEYRNGHOEV 60
QY 85 ESPFGRLQMGSKDLOVSTIVNTLNDGLTYCNVSRFEFEAHRPFV 135
DB 61 ESPFGRLQMGSKDLOVSTIVNTLNDGLTYCNVSRFEFEAHRPFV 111

RESULT 10

US-10-029-191-20
; Sequence 20, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:

; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/501
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 218

; TYPE: PRT
; ORGANISM: Lepus Sp.
US-10-029-191-20

Query Match 41.8%; Score 470.5; DB 13; Length 218;
Best Local Similarity 49.3%; Pred. No. 3.8e-39;
Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;

QY 6 RLPL-ASLVIIYWRVCPVCEVPSSETEAQGNPMKLRICSCMKREVEATTVVEM 62
DB 3 RLPAFVGAALVSGAM-----GCVEVDSSETEAQGNPMKLRICSCMKREVEATTVVEM 57
QY 63 FYRPEGKDFLIYEYRNGHOEVSP--FGRLQMGSK--KDLOVSTIVNTLNDGL 116
DB 58 TFQKGTBEFVKILRYENBVQLSEDERFEGRVVNGSRGKDLQDLISIFITVYTNHSG 117
QY 117 LYTCVSRFEFEAHRPFVKTTRLPLRYTEAGDEFTSVSEIMTYLLVFLTMFLIE 176
DB 118 DYQCHVYRLSFEYENHTSVYKKIHLEVDKARDMAISVSEIMTYLLVFLTMFLIE 177
QY 177 MIYCYRKYSKA--EBAQENASDYLAIPSENKEN 208
DB 178 MYCYKTIATAATEBAQENASEYLAIPSENKEN 210

RESULT 11

US-10-142-201B-8
; Sequence 8, Application US/10142201B
; Publication No. US20030022205A1
; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,
; FILE REFERENCE: MP12001-106P1RN(M)
; CURRENT APPLICATION NUMBER: US/10/142,201B
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/289,893
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-142-201B-8

Query Match 41.5%; Score 466.5; DB 14; Length 218;
Best Local Similarity 51.6%; Pred. No. 9.8e-39;
Matches 98; Conservative 28; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPSSETEAQGNPMKLRICSCMKREVEATTVVEMFYRPEGKDFLIYEYRNGHOEV 84
DB 21 CVEVDSSETEAQGNPMKLRICSCMKREVEATTVVEMFYRPEGKDFLIYEYRNGHOEV 80
QY 85 ESP--FGRLQMGSK--KDLOVSTIVNTLNDGLTYCNVSRFEFEAHRPFVKTTR 139
DB 81 EEDRFEGRVVNGSRGKDLQDLISIFITVYTNHSGDYECHVYRLLFEYENHTSVYK 140
QY 140 LIPLRYTEAGDEFTSVSEIMTYLLVFLTMFLIEMIYCYRKYSKA--EBAQENASDY 198
DB 141 KIHIEVDKARDMAISVSEIMTYLLVFLTMFLIEMIYCYKTIATAATEBAQENASEY 200
QY 199 LAIPSENKEN 208
DB 201 LAIPSENKEN 210

RESULT 12

US-10-477-272-2
; Sequence 2, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:

APPLICANT: Bionomics Limited
TITLE OF INVENTION: P12
FILE REFERENCE: SCN1B (P85C)
CURRENT APPLICATION NUMBER: US/10/477,272
CURRENT FILING DATE: 2003-11-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-477-272-2

Query Match 41.5%; Score 466.5; DB 16; Length 218;
Best Local Similarity 51.6%; Pred. No. 9.8e-39;
Matches 98; Conservative 28; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPSETEAVOQNPMLKRCISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84
DB 21 CVEVDSETEAVVGMTEFKILCISCKRSEETAETFTETFRQKGTBEFVKILRYENEVLQ 80
QY 85 ESP--FOGRIQWNGS---KLDQVSTVLTAVTNDGLTYCNVSRBEFFFAHRPFVKTTR 139
DB 81 EDECEGEGRYVWNGSGTKDLDLSIFITVTVNHSGDYECYHRYLLFFENYEHNTSVK 140
QY 140 LIPLRVTEAGEPFTSVSEIMMYILLVFLTLFLEMICYRKVSKA--EAAQENASDY 198
DB 141 KIHIEVVDKANRMASIVSEIMMYILLVLTILVLAEMICYKKAATAETAAQENASEY 200

QY 199 LAIPSENKEN 208
DB 201 LAITSESSEN 210

RESULT 13
US-09-977-579-44
Sequence 44, Application US/0977579
Publication No. US20040248240A1
GENERAL INFORMATION:
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
TITLE OF INVENTION: channel
TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
FILE REFERENCE: 674558-2001
CURRENT APPLICATION NUMBER: US/09/977,579
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/EP00/01783
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60,129,473
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 218
TYPE: PRT
ORGANISM: Rat
US-09-977-579-44

Query Match 41.2%; Score 463.5; DB 11; Length 218;
Best Local Similarity 51.1%; Pred. No. 2e-38;
Matches 97; Conservative 29; Mismatches 57; Indels 7; Gaps 4;

QY 26 CVEVPSETEAVOQNPMLKRCISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84
DB 21 CVEVDSETEAVVGMTEFKILCISCKRSEETAETFTETFRQKGTBEFVKILRYENEVLQ 80
QY 85 ESP--FOGRIQWNGS---KLDQVSTVLTAVTNDGLTYCNVSRBEFFFAHRPFVKTTR 139
DB 81 EDEBEREGRYVWNGSGTKDLDLSIFITVTVNHSGDYECYHRYLLFFENYEHNTSVK 140
QY 140 LIPLRVTEAGEPFTSVSEIMMYILLVFLTLFLEMICYRKVSKA--EAAQENASDY 198
DB 141 KIHIEVVDKANRMASIVSEIMMYILLVLTILVLAEMICYKKAATAETAAQENASEY 200

QY 199 LAIPSENKEN 208
DB 201 LAITSESSEN 210

RESULT 14
US-10-029-191-7
Sequence 7, Application US/10029191
Publication No. US20020160453A1
GENERAL INFORMATION:
APPLICANT: CURTIS, ROY A. J.
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
FILE REFERENCE: 210147.00XX/5U1
CURRENT APPLICATION NUMBER: US/10/029,191
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 09/569,978
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/134,198
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 58
TYPE: PRT
ORGANISM: Rattus sp.
US-10-029-191-7

Query Match 26.0%; Score 292; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.2e-22;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 SEIMMYILLVFLTLFLEMICYRKVSKAEEAQAQENASDYLAIPSENKENSVPVBE 215
DB 1 SEIMMYILLVFLTLFLEMICYRKVSKAEEAQAQENASDYLAIPSENKENSVPVBE 58

RESULT 15
US-09-875-456A-14
Sequence 14, Application US/09875456A
Patent No. US20020045229A1
GENERAL INFORMATION:
APPLICANT: Qln, Ning
APPLICANT: Codd, Ellen
TITLE OF INVENTION: D'Andrea, Michael
TITLE OF INVENTION: DNAs encoding human beta1a sodium channel subunit
FILE REFERENCE: ORT-1221
CURRENT APPLICATION NUMBER: US/09/875,456A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-456A-14

Query Match 22.9%; Score 257.5; DB 9; Length 268;
Best Local Similarity 44.7%; Pred. No. 1.7e-17;
Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 26 CVEVPSETEAVOQNPMLKRCISCKREVEATTVVEMFYRPEGKDFL-IYERYNGHOEV 84
DB 21 CVEVDSETEAVVGMTEFKILCISCKRSEETAETFTETFRQKGTBEFVKILRYENEVLQ 80
QY 85 ESP--FOGRIQWNGS---KLDQVSTVLTAVTNDGLTYCNVSRBEFFFAHRPFVKTTR 139
DB 81 EDEBEREGRYVWNGSGTKDLDLSIFITVTVNHSGDYECYHRYLLFFENYEHNTSVK 140
QY 140 LIPLRVTEAGE 151
DB 141 KIHIEVVDK-GE 151

Mon Apr 4 15:50:10 2005

us-09-977-579-1.rapb

Page 6

Search completed: March 31, 2005, 20:39:32
Job time : 92.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:10:33 ; Search time 26.5 Seconds

(without alignments)
780.627 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125

Sequence: 1 MPAFNRLLPLASLVLIYWR.....SDYLAIPSEKENSVPVEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 470.5 | 41.8 | 218 | 2 JC4788 | sodium channel pro |
| 2 | 466.5 | 41.5 | 218 | 2 A55734 | sodium channel, vo |
| 3 | 463.5 | 41.2 | 218 | 2 A42737 | sodium channel bet |
| 4 | 168 | 14.9 | 248 | 1 MPRT0 | myelin P0 protein |
| 5 | 164 | 14.6 | 248 | 1 JH0252 | myelin P0 protein |
| 6 | 164 | 14.6 | 251 | 2 I38053 | myelin protein zer |
| 7 | 162 | 14.4 | 219 | 1 A29128 | myelin P0 protein |
| 8 | 147.5 | 13.1 | 247 | 1 A54662 | myelin P0 protein |
| 9 | 145.5 | 12.9 | 246 | 1 A32999 | myelin P0 protein |
| 10 | 136 | 12.1 | 249 | 1 A61087 | myelin P0 glycopro |
| 11 | 113 | 10.0 | 215 | 2 A57843 | sodium channel bet |
| 12 | 112 | 10.0 | 186 | 2 I61783 | sodium channel bet |
| 13 | 109.5 | 9.7 | 1462 | 1 B36182 | protein-tyrosine-P |
| 14 | 107.5 | 9.6 | 820 | 2 S17295 | fibroblast growth |
| 15 | 107.5 | 9.6 | 821 | 1 TVM8BK | fibroblast growth |
| 16 | 106 | 9.4 | 800 | 1 TVH2F | fibroblast growth |
| 17 | 104 | 9.2 | 800 | 2 A48991 | heparin-binding gr |
| 18 | 104 | 9.2 | 801 | 2 I55363 | heparin-binding gr |
| 19 | 102.5 | 9.1 | 131 | 2 PT0178 | ig kappa chain pre |
| 20 | 101.5 | 9.0 | 129 | 2 S57884 | ig kappa chain pre |
| 21 | 101.5 | 9.0 | 131 | 2 B32513 | ig kappa chain pre |
| 22 | 101.5 | 9.0 | 131 | 2 B30577 | ig kappa chain pre |
| 23 | 101.5 | 9.0 | 353 | 2 S51232 | heparin-binding fi |
| 24 | 100.5 | 8.9 | 118 | 2 S24539 | ig kappa chain V r |
| 25 | 100.5 | 8.9 | 131 | 2 D34904 | ig kappa chain pre |
| 26 | 99.5 | 8.8 | 118 | 2 S24533 | ig kappa chain V r |
| 27 | 98.5 | 8.8 | 131 | 2 B39276 | ig light chain pre |
| 28 | 98.5 | 8.8 | 2 | A35963 | protein-tyrosine k |
| 29 | 98 | 8.7 | 130 | 2 C29380 | ig kappa chain pre |

| | | | | | |
|----|------|-----|-----|----------|--------------------|
| 30 | 98 | 8.7 | 372 | 2 C39371 | ig V-region-like B |
| 31 | 97 | 8.6 | 136 | 2 S36320 | T-cell receptor de |
| 32 | 96.5 | 8.6 | 118 | 2 S24535 | ig kappa chain V r |
| 33 | 96.5 | 8.6 | 118 | 2 S24500 | ig kappa chain V r |
| 34 | 96.5 | 8.6 | 118 | 2 S24529 | ig kappa chain V r |
| 35 | 96.5 | 8.6 | 131 | 2 B34904 | ig kappa chain pre |
| 36 | 96.5 | 8.6 | 131 | 2 S09259 | ig kappa chain pre |
| 37 | 95.5 | 8.5 | 118 | 2 S24507 | ig kappa chain V r |
| 38 | 95.5 | 8.5 | 112 | 2 PH0106 | anti-digoxin trans |
| 39 | 95.5 | 8.5 | 750 | 2 S41051 | fibroblast growth |
| 40 | 95.5 | 8.5 | 821 | 1 TVHUF2 | fibroblast growth |
| 41 | 95.5 | 8.5 | 898 | 2 A40114 | fasciclin II precu |
| 42 | 94.5 | 8.4 | 118 | 2 S24536 | ig kappa chain V r |
| 43 | 94.5 | 8.4 | 118 | 2 S24503 | ig kappa chain V r |
| 44 | 94.5 | 8.4 | 118 | 2 S24508 | ig kappa chain V r |
| 45 | 94.5 | 8.4 | 118 | 2 S24532 | ig kappa chain V r |

ALIGNMENTS

```

RESULT 1
JC4788
sodium channel protein betal chain - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4788
R:Belcher, S.M.; Howe, J.R.
Gene 170, 285-286, 1996
A:Title: Cloning of the cDNA encoding the sodium channel betal subunit from rabbit.
A:Reference number: JC4788; PMID:9625151; PMID:8666261
A:Accession: JC4788
A:Molecule type: mRNA
A:Residues: 1-218 <BEL>
A:Cross-references: UNIPROT:P53788; GB:U35382; NID:G1016013; PIDN:AAB17572.1; PID:G1016013
C:Comment: This protein is composed of a large alpha-chain and two small beta-chains and
duction.
C:Genetics:
A:Gene: Odetal
C:Keywords: glycoprotein; membrane protein; muscle; transmembrane protein
F:161-182/Domain: transmembrane #status predicted <TM>
F:93,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      41.8%; Score 470.5; DB 2; Length 218;
Best Local Similarity 49.3%; Pred. No. 5.8e-34;
Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;

QY      6 RLPL- --ASLVLIYWRVCFPVCEVPSFETAVVQGNPMKLRICISCKREVEATTVVEM 62
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      3 RLALFVVGALVSSAM- ---GGCEVDSETEAVGKTFKILCISCKRSETTAETFEW 57
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      63 FYRPEGKDFL-IYERYNGHOEVESP--FOGRLOWNGS--KDLQDVSTLVNVLNDSG 116
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      58 TFRQKGTETFEVKLRARENEDVQLQEBDEPRGKRVVWNGSRGTXLDLSDITVTWYHSG 117
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      117 LYTCNVSRFEFFAHRRPFYKTRLLPLRVTEEGEFTSVSSIMYILVFLTWFIE 176
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      118 DYQCHVYRLLSFENYENHTSVVKRIHLEVVDKKNRMWASISIMYVLTIVLTVLVAE 177
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      177 MYCYRKVSKA--EEAQAENASDYLAIPESENK 208
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      178 MYCYRKIAATATAAQAENASEYLAITSESEN 210
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 2
A55734
sodium channel, voltage-gated, beta-1 chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55734; A53408; I54354
R:Makita, N.; Sloan-Brown, K.; Weghuis, D.O.; Rogers, H.H.; George Jr., A.L.
Genomics 23, 628-634, 1994
A:Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)

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[illegible]

| Matches | 97; Conservative | 29; Mismatches | 57; Indels | 7; Gaps | 4; |
|---------|------------------|--|------------|---------|----|
| Qy | 26 | CVEVPSEIEAQQGPMKLRCTSCMKREBEVLTIVEMVYRPEGKDFL-IYEYRNGHEV | 84 | | |
| Db | 21 | CVEADSEIEAYGTMFKILCISCKRSETTAETETEMTFROKGTBEFKIIRYENVLQ | 80 | | |
| Qy | 85 | ESP--FQGRLOWNGS---KDLQDVSIYLVANTLNDSGLYTGNVSRREEFEAHRPFVKTR | 139 | | |
| Db | 81 | EEDRFESRIVVMNNSRGTQDLQDLSIFLTNTVTHNSGDYEHVYRLLEFDNYEHNTSVVK | 140 | | |
| Qy | 140 | LIPLRVTEAGEDPTSVYSEIMMTITLLVFLTLMFIEMTYCYRYKYSKA-EELAQENASDY | 198 | | |
| Db | 141 | KIHIEVVDKARNDMASIVSEIMMYVLLIVLITLVAENKVCYKXIIAATAEAAQENASEY | 200 | | |
| Qy | 199 | LAIPSENKEN 208 | | | |
| Db | 201 | LAITSEKEN 210 | | | |

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RESULT 4
MERT0
myelin P0 protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1987 #sequence _revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: J00622; A22822
R:Lenke, G.; Lamar, E.; Patterson, J.
Neuron 1, 73-83, 1988
A:Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.
A:Reference number: J00622; MUID:90164482; PMID:2483091
A:Accession: J00622
A:Molecule type: DNA
A:Residues: 1-248 <LEM>
A:Cross-references: UNIPROT:P06907
R:Lenke, G.; Axel, R.
Cell 40, 501-508, 1985
A:Title: Isolation and sequence of a cDNA encoding the major structural protein of perip
A:Reference number: A22822; MUID:85124601; PMID:2578885
A:Accession: A22822
A:Molecule type: mRNA
A:Residues: 1-248 <LEM2>
C:Comment: This protein is found only in peripheral nervous system Schwann cells.
C:Genetics:
A:Introns: 23/1; 78/3; 150/1; 195/2; 215/3
C:Superfamily: myelin P0 protein; immunoglobulin homology
C:Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protei
E:1-29/Domain: signal sequence #status predicted <SIG>
F:30-248/Product: myelin P0 protein #status predicted <MAT>
F:30-153/Domain: extracellular #status predicted <EXD>
F:43-129/Domain: immunoglobulin homology <IMW>
F:154-179/Domain: transmembrane #status predicted <TMD>
F:180-248/Domain: intracellular #status predicted <IND>
F:122/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 14.9%; Score 168; DB 1; Length 248;
Best Local Similarity 27.2%; Pred. No. 2,3e-07;
Matches 58; Conservative 35; Mismatches 102; Indels 18; Gaps 7;

QY 8 LPLASLVIYWMVRCFVCEVPEVPSFEAVQGNPMKRCISCMKREEVEATTVMFYRPE 67
DB 17 LIFSSVLV-----SPLTALIVYTRDREYVAGVSVTLIHC-SFMSSEWVSDDISTFWKYDPE 71

QY 68 GSKDFL-IVYENGHOEVE--SPFOGRLQWNSKDLQDVSIITVANTLNDGJYTCNVR 124
DB 72 GGRDAISIFHYAKGGPYIDVEGTFPKERIGWMBDSMKDGSIVIHNDYSDNGTFCDVKN 131

QY 125 EPEFAHRPFPVKTLLIPLRVTEAGEDFTSVSSEIMATIL-LVFETLMFIEMITCYRK 183
DB 132 PPD-----IVGKTSQVTLVYFEKVPTRGYGVILGAVIGILGVLLLLLFYLIRYCMWR 185

QY 184 VSKAE---AAQENASDYLAIPSENKENSVVY 213
DB 186 ROALQORLSAMEKGRFKKSSKDSGRGRQTV 218

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RESULT 5

JH0252
 myelin P0 protein precursor - human
 N:Alternate names: myelin protein zero
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence, revision 06-Dec-1996 #text_change 09-Jul-2004
 C:Accession: JH0252; JN0704; J39378; I58118
 R:Hayasaka, K.; Nanno, K.; Tanahara, M.; Sato, W.; Takada, G.; Mura, M.; Uemura, K.
 Biochem. Biophys. Res. Commun. 180, 515-518, 1991
 A:Title: Isolation and sequence determination of cDNA encoding the major structural prot
 A:Reference number: JH0252; MUID:92062068; PMID:171967
 A:Accession: JH0252
 A:Molecule type: mRNA
 A:Residues: 1-248 <HA>
 A:Cross-references: UNIPROT:P25189; GB:D10537; GB:D90501; NID:9220073; PIND:BA01395.1;
 A:Experimental source: fetus spinal cord
 R:Hayasaka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Mura, Y.
 Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993
 A:Title: Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy type 1.
 A:Reference number: JN0704; MUID:93356807; PMID:7668964
 A:Accession: JN0704
 A:Molecule type: mRNA
 A:Residues: 1-248 <HA2>
 R:Pham-Dinh, D.; Fourtbl, Y.; Blanquet, F.; Mattei, M.G.; Roeckel, N.; Latour, P.; Chaz
 Hum. Mol. Genet. 2, 2051-2054, 1993
 A:Title: The major peripheral myelin protein zero gene: structure and localization in th
 A:Reference number: J39378; MUID:94154677; PMID:7509228
 A:Accession: J39378
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-248 <RES>
 A:Molecule type: DNA
 A:Cross-references: GB:I24893; NID:9454412; PIND:AAA20656.1; PID:9529405
 R:Kulkarni, T.; Bolhuis, P.A.; Wolterman, R.A.; Kemp, S.; de Nijhuis, S.; Valentijn, L.
 Nature Genet. 5, 35-39, 1993
 A:Title: Deletion of the serine 34 codon from the major peripheral myelin protein P0 ge
 A:Reference number: I58118; MUID:94035114; PMID:7693130
 A:Accession: I58118
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-62,64-115 <RES2>
 A:Cross-references: GB:S66705; NID:9437048; PIND:AA828708.1; PID:9437049
 A:Experimental source: disease-state mutant
 C:Comment: This protein, a small integral membrane glycoprotein, is the most abundant pr
 C:Comment: This protein plays essential roles in both the elaboration and the subsequent
 C:Gene: GDB:MP2; CMT1B; CMT1B; HMSNIB
 A:Gene: GDB:MP2; CMT1B; CMT1B; HMSNIB
 A:Cross-references: GDB:125266; OMIM:159440
 A:Map position: 1q22-1q23
 A:Introns: 23/1; 78/3; 150/1; 195/2; 215/3
 C:Superfamily: myelin P0 protein; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
 F:1-29/Domains: signal sequence #status predicted <SIG>
 F:30-248/Product: peripheral myelin #status predicted <SIG>
 F:43-129/Domains: immunoglobulin homology <IMM>
 F:50-127/Domains: immunoglobulin homology <IMM>
 F:122/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 164; DB 1; Length 248;
 Best Local Similarity 27.7%; Pred. No. 5.2e-07;
 Matches 53; Conservative 34; Mismatches 82; Indels 22; Gaps 7;
 QY 14 VLIYWRVCFP---VCVEVSETEAVOAGNPMKRCISCMKEVEATVTEVFRPBGK 70
 DB 16 VLFSSLVSPAPAIYVYTDREYHGAAGSRVTLHC-SFMSSEVSDISFTWRYOPEGGR 74
 QY 71 DFLIYEYRNGHOVE--SPFOGRLOMNGSKDLQDVSTVLTNTLDSGLYTCNVSRPE 127
 DB 75 DAISITHYAKGQYIDVGVGFKERIQWGDPRMKDGSIVHNDYSDNGFTCDVKNPPD 134
 QY 128 FEARFPVKTRLLIPRVTEAGEDFTSVSEIMMTIL-LVFLTLWLFEMICY----- 181
 DB 135 -----IVGTSQVTLVPEKVPTRYGAVIGVGLVLLLLLFYVVRGWLRRQA 188

RESULT 6

myelin protein zero - human
 C:Species: Homo sapiens (man)
 C>Date: 17-May-1996 #sequence, revision 17-May-1996 #text_change 09-Jul-2004
 C:Accession: I38053; A49643; S43191
 R:Rautenstrauss, B.; Nellis, E.; Gehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.
 Hum. Mol. Genet. 3, 1701-1702, 1994
 A:Title: Identification of a de novo inactivating mutation in P0 in a patient with a Dejer
 A:Reference number: I38053; MUID:95135435; PMID:7530550
 A:Accession: I38053
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-251 <RES>
 A:Cross-references: UNIPROT:Q14902; EMBL:Z31718; NID:9469516; PIND:CAA83513.1; PID:946951
 R:Su, Y.; Brooks, D.G.; Li, L.; Lepercq, U.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993
 A:Title: Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients.
 A:Reference number: A49643; MUID:94068501; PMID:7504284
 A:Accession: A49643
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 50-105 <SU1>
 A:Experimental source: peripheral blood
 A:Note: sequence extracted from NCBI backbone (NCBIP.139777)
 C:Gene: GDB:MP2; CMT1B; CMT1
 A:Gene: GDB:MP2; CMT1B; CMT1
 A:Cross-references: GDB:125266; OMIM:159440
 A:Map position: 1q22-1q23
 C:Superfamily: myelin P0 protein; immunoglobulin homology
 F:43-129/Domains: immunoglobulin homology <IMM>

Query Match 14.6%; Score 164; DB 2; Length 251;
 Best Local Similarity 27.7%; Pred. No. 5.2e-07;
 Matches 53; Conservative 34; Mismatches 82; Indels 22; Gaps 7;

QY 14 VLIYWRVCFP---VCVEVSETEAVOAGNPMKRCISCMKEVEATVTEVFRPBGK 70
 DB 16 VLFSSLVSPAPAIYVYTDREYHGAAGSRVTLHC-SFMSSEVSDISFTWRYOPEGGR 74
 QY 71 DFLIYEYRNGHOVE--SPFOGRLOMNGSKDLQDVSTVLTNTLDSGLYTCNVSRPE 127
 DB 75 DAISITHYAKGQYIDVGVGFKERIQWGDPRMKDGSIVHNDYSDNGFTCDVKNPPD 134
 QY 128 FEARFPVKTRLLIPRVTEAGEDFTSVSEIMMTIL-LVFLTLWLFEMICY----- 181
 DB 135 -----IVGTSQVTLVPEKVPTRYGAVIGVGLVLLLLLFYVVRGWLRRQA 188
 QY 182 ---RKVSKAE 189
 DB 189 ALQRLSAMEK 199
 RESULT 7
 A29128
 myelin P0 protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A29128
 R:Sakamoto, Y.; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uemura, K.
 J. Biol. Chem. 262, 4208-4214, 1987
 A:Title: Complete amino acid sequence of P0 protein in bovine peripheral nerve myelin.
 A:Reference number: A29128; MUID:87166035; PMID:2435734
 A:Accession: A29128
 A:Molecule type: protein
 A:Residues: 1-219 <SAK>
 A:Cross-references: UNIPROT:P10522

C:Superfamily: myelin P0 protein; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein; myelin; phosphoprotein; Schwann cell; struct
 F:14-100/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 162; DB 1; Length 219;

Best Local Similarity 26.5%; Pred. No. 6.7e-07; Indels 14; Gaps 6;
 Matches 52; Conservative 32; Mismatches 98;

QY 25 VCEVPSETEAVQGNPKLRICISCKRREVEATTVEMFYRPEGKDFL-IYEYRNGHOE 83
 DB 1 IVVYIDKEVHGAVGQVTLTC-SFWSSEWVSDLSFTWRYPGEGRDALISIFHYAKGQPY 59
 QY 84 VE--SPFGRLQWNGSKDLQDVSTVLNVTLNDGLYCNVSRFEFEARHPVKTTRLI 141
 DB 60 IDEVGTFFKRIQWVDPRKDGSIYIHNDYGDNGTFTCDVKNPPD-----IVGKTSQV 113
 QY 142 PLRVTEAGEDFTSVSEIMYIL-LVFLTLMLFLEMICYKVKAKABA---AQENMSD 197
 DB 114 TLVFEKVPTRYGVALGAVIGVLLALLFLYLIRICWLRQAALQRLHAMEKGL 173
 QY 198 YLAIPSENKENVVPV 213
 DB 174 HKTAKDASGRGRTPV 189

RESULT 8

A54662

myelin P0 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000

C:Accession: A54662

R.You, K.H.; Heisler, C.L.; Hayes, C.; Stahl, N.; Francke, U.; Popko, B.

Genomics 9, 751-757, 1991

A>Title: DNA sequence, genomic organization, and chromosomal localization of the mouse P

A:Reference number: A54662; MUID:9M244320; PMID:1709914

A:Accession: A54662

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <YOU>

A:Cross-references: GB:M62427

C:Superfamily: myelin P0 protein; immunoglobulin homology

F:43-128/Domain: immunoglobulin homology <IMM>

Query Match 13.1%; Score 147.5; DB 1; Length 247;

Best Local Similarity 26.8%; Pred. No. 1.4e-05;

Matches 57; Conservative 35; Mismatches 102; Indels 19; Gaps 8;

QY 8 LPLASLVLYIWRVCPVCEVPESETEAVQGNPKLRICISCKRREVEATTVEMFYRPE 67
 DB 17 LFFSLVLT----SPALAIVYTDREIYGAVGQVTLHC-SFWSSEWVSDLSFTWRYPQ-E 70
 QY 68 GGDPL-IYEYRNGHOEVE--SPFOGRLQWNGSKDLQDVSTVLNVTLNDGLYCNVSR 124
 DB 71 GGRDIALSFHYAKGQPYIDVCAFKERIQWVDPRKDGSIYIHNDISDNGTFTCDVKN 130
 QY 125 EEFEPARHPVKTTRLIPLRVTEAGEDFTSVSEIMYIL-LVFLTLMLFLEMICYRK 183
 DB 131 PPD-----IVGKTSQVTLVFEKVPTRYGVALGAVIGVLLALLFLYLIRICWLR 184
 QY 184 VSKAE---AQENMSDYLAIPSENKENVVPV 213
 DB 185 RQAALQRLHAMEKGRFHKSSKSSKRGRTPV 217

RESULT 9

A52999

myelin P0 protein precursor - horn shark

C:Species: Heterodontus francisci (horn shark)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A52999

R.Savedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, J.

Mol. Evol. 23, 149-156, 1989

A>Title: The myelin proteins of the shark brain are similar to the myelin proteins of ch

A:Reference number: A52999; MUID:90040744; PMID:2478717

A:Accession: A52999

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 <SAA>

A:Cross-references: UNIPROT:P20938; GB:X16714; NID:963976; PIDN:CAB37865.1; PID:94467434

C:Superfamily: myelin P0 protein; immunoglobulin homology

C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein

F:41-127/Domain: immunoglobulin homology <IMM>

Query Match 12.9%; Score 145.5; DB 1; Length 246;

Best Local Similarity 25.8%; Pred. No. 2.1e-05;

Matches 49; Conservative 37; Mismatches 77; Indels 27; Gaps 7;

QY 16 IYWRVCPVCEVPESETEAVQ-----GNPKLRICISCKRREVEATTVEMFYR 66
 DB 10 LFCCSVLAFAPVLNRSGISVSTHNNHKYGVSDVTLTC-GFWSNEVYSDLTLSMRFRP 68
 QY 67 EGGKDFL-IYEYRNGHOEVE--SPFGRLQWNGSKDLQDVSTVLNVTLNDGLYCNV 123
 DB 69 DNSRDIISIFHYGNGVPIEKGQFRGRVWVGDISKDGSIIVIRNLDIINGTFTCDVK 128
 QY 124 REFEARHPVKTTRLIPLRVTEE-----AGEDFTSVSEIMYILVFLTLMLFEMI 178
 DB 129 NPPD-----VVGTSDDVLTVDKIPVAGVVSAGATIGFLGILLVGGLYF---R 179
 QY 179 YCYRKVSRAE 188
 DB 180 YIVRRARAE 189

RESULT 10

A61087

myelin P0 glycoprotein precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A61087

R. Barbu, M.

J. Neurosci. Res. 25, 143-151, 1990

A>Title: Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for earl

A:Reference number: A61087; MUID:90204597; PMID:1690817

A:Accession: A61087

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-249 <BAR>

A:Cross-references: UNIPROT:P37301

C:Comment: This protein is found only in peripheral nervous system Schwann cells.

C:Superfamily: myelin P0 protein; immunoglobulin homology

C:Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protei

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-249/Product: myelin P0 glycoprotein #status predicted <MAT>

F:43-129/Domain: extracellular #status predicted <EXT>

F:154-179/Domain: immunoglobulin homology <IMM>

F:180-249/Domain: transmembrane #status predicted <TM>

F:122/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 12.1%; Score 136; DB 1; Length 249;

Best Local Similarity 23.9%; Pred. No. 0.00015;

Matches 44; Conservative 38; Mismatches 82; Indels 20; Gaps 7;

QY 27 VEVPSETEAVQGNPKLRICISCKRREVEATTVEMFYRPEGKDFL-IYEYRNGHOEVE 85
 DB 32 VYTPREVYGTGSHVTLSC-SFWSSEWVSDLSFTWRYPGEGRDALISIFHYGQPYID 90
 QY 86 --SPFGRLQWNGSKDLQDVSTVLNVTLNDGLYCNVSRFEFEARHPVKTTRLIPL 143
 DB 91 DVGSFEKEMEWGNRRKDGSIYIHNDYTDNGTFTCDVKNPPD-----IVGSSQVTL 144
 QY 144 RVTEAGEDFTSVSEIMYILVFLTLMLFEMI-YCY-----RKVKAKABA-AQE 193
 DB 145 YLVEKVPTRYGVALGAVIGVLLALLVAVVAVVVRFCWLRQAALQRLHAMEKGLQR 204

QY 194 NASD 197
Db 205 SAKD 208

RESULT 11
A57843
Sodium channel beta 2 subunit - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: A57843
R/Isom: L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeck, R.E.; Reber, B.F.X.; Scheuer, C.
Cell 83, 433-442, 1995
A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein
A/Reference number: A57843; PMID:96067641; PMID:8521473
A/Accession: A57843
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-215 <RES>
A/Cross-references: UNIPROT:P54900; EMBL:U37026; NID:g1086496; PIDN:AA052967.1; PID:g1086496
C/Genetics:
A/Genes: SCN2

Query Match 10.0%; Score 113; DB 2; Length 215;
Best Local Similarity 25.3%; Pred. No. 0.013;
Matches 47; Conservative 39; Mismatches 80; Indels 20; Gaps 8;

QY 27 VEPSTBAVQGNPKLRCT--SCMKREVEATTVMFPRPGG--KDFLIYFRNGH 81
Db 32 VVPTPLSLVANGSDTRLPCTFNSCYVNHQFS--LMTVQECNCSSEMFLOFRMKIN 89
QY 82 OEVSPPQGLONGSKDLDVGSITVLTNTLNDGLTCNVSEFEFAHFPVKTTRLI 141
Db 90 LKLER-FGDRVERSGNPSKIDSVTLKNVQLEDEGINCTIN--PPDRHGHGK---1 142
QY 142 PLRVTSEAGDFTSVSEIMVYLVLFLTLMLFLEMV--CYRKYSKAEAAQENASDYLA 200
Db 143 YLQVLLVPPERDSTVAIVIGASVGFLLAVIILVMVKCVRR----KKEQLSTDDDK 197
QY 201 IPSENK 206
Db 198 TEEBCK 203

RESULT 12
161783
Sodium channel beta 2 subunit - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C/Accession: I61783
R/Isom: L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeck, R.E.; Reber, B.F.X.; Scheuer, C.
Cell 83, 433-442, 1995
A/Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein
A/Reference number: A57843; PMID:96067641; PMID:8521473
A/Accession: I61783
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-186 <RES>
A/Cross-references: UNIPROT:Q62861; EMBL:U37147; NID:g1086498; PIDN:AA060506.1; PID:g1086498
C/Genetics:
A/Genes: SCN2
A/Introns: 50/3; 120/2

Query Match 10.0%; Score 112; DB 2; Length 186;
Best Local Similarity 24.1%; Pred. No. 0.014;
Matches 47; Conservative 36; Mismatches 74; Indels 38; Gaps 8;

QY 27 VEPSTBAVQGNPKLRCT--SCMKREVEATTVMFPRPGGKDFLIYFRNGH 84
Db 3 VVPTPLSLVANGSDTRLPCTFNSCYVNHQFS--LMTVQ-----ECNSCSSEEM 50
QY 85 EEPQ-----GRLQNGSKDLDVGSITVLTNTLNDGLTCNVSEFEFAH 132

Db 51 VLQPRMKIINLKLEREGDRVPSGNPSKYDVSTLKNVQLEDEGINCYITN--PPDRHR 108
QY 133 PFVKTTRLPLRTEREAGEFTSVSEIMVYLVLFLTLMLFLEMV--CYRKYSKAEAA 191
Db 109 GHGK---YLQVLLVPPERDSTVAIVIGASVGFLLAVIILVMVKCVRR----KKE 159
QY 192 QENASDYLAIPSENK 206
Db 160 QKSTDDDKTEEBCK 174

RESULT 13
B36182
N/Alternate names: protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type PTP69D precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: B36182
R/Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989
A/Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila
A/Reference number: A36182; PMID:90046860; PMID:2554325
A/Accession: B36182
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1462 <STR>
A/Cross-references: UNIPROT:P16620; GB:M27699; NID:g158188; PIDN:AAA28842.1; PID:g158188
C/Genetics:
A/Genes: Ptp69D
A/Cross-references: FlyBase:FBgn014007
C/Superfamily: protein-tyrosine-phosphatase, receptor type PTP69D; fibronectin type III; phosphatase homology
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; signal sequence; status predicted <SIG>
F/1-28/Domain: signal sequence #status predicted <SIG>
F/29-1462/Product: protein-tyrosine-phosphatase, receptor type PTP69D #status predicted <EXT>
F/29-806/Domain: extracellular #status predicted <EXT>
F/38-114/Domain: immunoglobulin homology <IM1>
F/147-216/Domain: immunoglobulin homology <IM2>
F/807-823/Domain: transmembrane #status predicted <TM>
F/824-1462/Domain: intracellular #status predicted <INT>
F/917-1145/Domain: protein-tyrosine-phosphatase homology <PTP1>
F/1213-1439/Domain: protein-tyrosine-phosphatase homology <PTP2>
F/44-112, 154-214/Disulfide bonds: #status predicted
F/1097/Active site: Cys (phosphocysteine intermediate) #status predicted
F/1103/Binding site: substrate phosphate (Arg) #status predicted
F/1391/Active site: Cys (phosphocysteine intermediate) #status predicted
F/1397/Binding site: substrate phosphate (Arg) #status predicted

Query Match 9.7%; Score 109.5; DB 1; Length 1462;
Best Local Similarity 26.7%; Pred. No. 0.22; Indels 37; Gaps 11;
Matches 47; Conservative 31; Mismatches 61; Indels 37; Gaps 11;

QY 4 FNNLPLSLVILYVWVCFVCEVSETE-AVQGNPKLRCTSCMKREVEATTVM 62
Db 5 YRMSMLNIIILAY-IFLC-AICVQSVQVQMAEIKNLSBAS-----ENNA---VW 54
QY 63 FPRPEG-GKDFLIYFRNGHQEVSPPQGLONGSKDLDVGSITVLTNTLNDG 116
Db 55 KLGNQITINKNHPFYKIRT-----EPLKNDGSENNDSQDFMKYKNVTLTLDVNNDSG 108
QY 117 LYTC-----NYSREFEFAHFPVKTTRLPLRTEREAGEFTSVSEIMVYL 166
Db 109 NYCTAQTQGNHSTEFQVRYLP-SKVLQSTPDRIRKIKQD-----VMLYCLT 156

RESULT 14
S17295
fibroblast growth factor receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S17295
R/Raz, V.; Kaiman, Z.; Avioli, A.; Neufeld, G.; Givol, D.; Yarden, Y.
Oncogene 6, 753-760, 1991

A>Title: PCR-based identification of new receptors: molecular cloning of a receptor for
 A:Accession: S17295; MUID:91270892; PMID:1711190
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-820 <RAZ>
 A:Cross-references: UNIPROT:P21803; EMBL:X55441; NID:G50141; PID:CAA39083.1; PID:G50142
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
 F:270-343/Domain: immunoglobulin homology <IMM>
 F:478-763/Domain: protein kinase homology <KIN>

Query Match 9.6%; Score 107.5; DB 2; Length 820;
 Best Local Similarity 25.9%; Pred. No. 0.17;

Matches 41; Conservative 22; Mismatches 56; Indels 39; Gaps 7;

QY 83 EVESPFQGRLOW-----NGSK-----DIQDVSIYV---NVTLNDG 116
 DB 278 KYSDAQPHIQIKVEKNGSKYGPDLPLKVLKAGVNTTDEKEIVLYIRNVTFEEDAG 337
 QY 117 LYTCVNSREFEFAHRPVPKTRLLPLRYTE-EAGEDFTSVSEIMWYLLVFLTLMLFI 175
 DB 338 EYTLAAGNSIGISFHSAML-TVLPAPVREKEITLSPDYL---EIAICIGVFLIACWV 392
 QY 176 EMICYRKVSKAEBAQENASDYLAIPSENKENSVPV 213
 DB 393 TVIFCRMKTTTK-----PDFSSQPAVHKLTRIPL 423

RESULT 15

TVMSBK

fibroblast growth factor receptor bek precursor - mouse

N:Alternate names: bek transforming protein; fibroblast growth factor receptor 2; kerati
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112) bek

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1991 #sequence revision 13-Mar-1997 #text change 09-Jul-2004

C:Accession: A41142; A31378

R:Mansukhani, A.; Dell'Era, P.; Moscatelli, D.; Kornbluth, S.; Hanafusa, H.; Basilio, C

Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992

A>Title: Characterization of the murine BEK fibroblast growth factor (FGF) receptor: act

A:Reference number: A41142; MUID:92228773; PMID:1373495

A:Accession: A41142

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-821 <MAN>

A:Cross-references: UNIPROT:P21803; GB:M86441

R:Kornbluth, S.; Paulson, K.E.; Hanafusa, H.

Mol. Cell. Biol. 8, 5541-5544, 1988

A>Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA

A:Reference number: A31378; MUID:89219016; PMID:2468999

A:Accession: A31378

A:Molecule type: mRNA

A:Residues: 477-821 <KOR>

A:Cross-references: GB:M23362; NID:G533219; PIDN:AAA37285.1; PID:G533220

C:Genetics:

A:Gene: bek

C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;

F:1-21/Domain: signal sequence #status predicted <SIG>

F:122-821/Product: fibroblast growth factor receptor bek #status predicted <MAT>

F:117-233/Domain: immunoglobulin homology <IMM>

F:178-398/Domain: transmembrane #status predicted <TM>

F:479-764/Domain: protein kinase homology <KIN>

F:487-495/Region: protein kinase ATP-binding motif

F:62-107-179-231, 278-343/Dissulfide bonds: #status predicted

F:83, 123, 147, 241, 265, 297, 318, 331/Binding site: carbohydrate (asn) (covalent) #status pre

F:517, 534, 626/Active site: Lys, Glu, Asp #status predicted

F:657/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 9.6%; Score 107.5; DB 1; Length 821;
 Best Local Similarity 25.9%; Pred. No. 0.17;

Matches 41; Conservative 22; Mismatches 56; Indels 39; Gaps 7;

QY 83 EVESPFQGRLOW-----NGSK-----DIQDVSIYV---NVTLNDG 116

DB 279 KYSDAQPHIQIKVEKNGSKYGPDLPLKVLKAGVNTTDEKEIVLYIRNVTFEEDAG 338
 QY 117 LYTCVNSREFEFAHRPVPKTRLLPLRYTE-EAGEDFTSVSEIMWYLLVFLTLMLFI 175
 DB 338 EYTLAAGNSIGISFHSAML-TVLPAPVREKEITLSPDYL---EIAICIGVFLIACWV 393
 QY 176 EMICYRKVSKAEBAQENASDYLAIPSENKENSVPV 213
 DB 394 TVIFCRMKTTTK-----PDFSSQPAVHKLTRIPL 424

Search completed: March 31, 2005, 20:22:48
 Job time : 28.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:02:27 ; Search time 116 seconds
(without alignments)
949.112 Million cell updates/sec

Title: US-09-977-579-1

Perfect score: 1125

Sequence: 1 MPAPFRLPLASLVLYWVR.....SDYLAIPEKNSVYVBE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 1125 | 100.0 | 215 | 1 | CIB3_RAT | 09jko0 rattus norv |
| 2 | 1117 | 99.3 | 215 | 1 | CIB3_MOUSE | 08bhz3 mus musculu |
| 3 | 1117 | 99.3 | 268 | 2 | 069203 | 0892q3 mus musculu |
| 4 | 1105 | 98.2 | 215 | 1 | CIB3_HUMAN | 09ny72 homo sapien |
| 5 | 1097 | 97.5 | 215 | 1 | CIB3_MACFA | 08hx77 macaca fasc |
| 6 | 700 | 62.2 | 215 | 2 | 06DE47 | 06de47 xenopus lae |
| 7 | 470.5 | 41.8 | 218 | 1 | CIB1_RABIT | P33788 oryctolagus |
| 8 | 466.5 | 41.5 | 218 | 1 | CIB1_HUMAN | 007699 homo sapien |
| 9 | 463.5 | 41.2 | 218 | 1 | CIB1_RAT | 000954 rattus norv |
| 10 | 461 | 41.0 | 218 | 1 | CIB1_MOUSE | P97952 mus musculu |
| 11 | 419.5 | 37.3 | 186 | 2 | 08WU42 | 08wu42 homo sapien |
| 12 | 257.5 | 22.9 | 273 | 2 | 06TN97 | 06tn97 homo sapien |
| 13 | 257.5 | 22.9 | 273 | 2 | 09OXU3 | 09oxu3 rattus norv |
| 14 | 204.5 | 18.2 | 66 | 2 | 06L866 | 06l866 rattus norv |
| 15 | 175.5 | 15.6 | 203 | 2 | 08URF6 | 08urf6 brachydanio |
| 16 | 168 | 14.9 | 248 | 1 | MYPO_RAT | P06907 rattus norv |
| 17 | 165 | 14.7 | 248 | 1 | MYPO_MOUSE | P27573 mus musculu |
| 18 | 164 | 14.6 | 248 | 1 | MYPO_HUMAN | P25189 homo sapien |
| 19 | 164 | 14.6 | 251 | 2 | 014902 | 014902 homo sapien |
| 20 | 163.5 | 14.5 | 248 | 2 | 06W8B5 | 06w8b5 equus cabal |
| 21 | 163 | 14.5 | 209 | 2 | 06DDH9 | 06ddh9 xenopus lae |
| 22 | 162 | 14.4 | 219 | 1 | MYPO_BOVIN | P10522 bos taurus |
| 23 | 153 | 13.6 | 202 | 2 | 091406 | 091406 salmo sp. 1 |
| 24 | 152 | 13.5 | 235 | 2 | 06UWV2 | 06uwv2 homo sapien |
| 25 | 151 | 13.4 | 215 | 2 | 06NW73 | 06nw73 brachydanio |
| 26 | 150 | 13.3 | 215 | 2 | 091WI4 | 091wi4 mus musculu |
| 27 | 150 | 13.3 | 215 | 2 | 091WI4 | 091wi4 mus musculu |
| 28 | 147.5 | 13.1 | 215 | 1 | EVAI_HUMAN | O60487 homo sapien |
| 29 | 145.5 | 12.9 | 246 | 1 | MYPO_HERFR | P20938 heterodontu |
| 30 | 142.5 | 12.7 | 229 | 2 | 08AVM3 | 08avm3 xenopus lae |
| 31 | 136 | 12.1 | 249 | 1 | MYPO_CHICK | P37301 gallus gall |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 32 | 132.5 | 11.8 | 270 | 2 | 06AYT8 | 06ayt8 rattus norv |
| 33 | 131 | 11.6 | 243 | 2 | 09UEL4 | 09uel4 homo sapien |
| 34 | 131 | 11.6 | 269 | 2 | 095297 | 095297 homo sapien |
| 35 | 126.5 | 11.2 | 209 | 2 | 06GQX5 | 06gqx5 mus musculu |
| 36 | 124.5 | 11.1 | 199 | 2 | 08UG36 | 08ug36 brachydanio |
| 37 | 123 | 10.9 | 183 | 2 | 09UEL6 | 09uel6 homo sapien |
| 38 | 123 | 10.9 | 209 | 2 | 09NYK4 | 09nyk4 homo sapien |
| 39 | 123 | 10.8 | 202 | 2 | 08IX11 | 08ix11 homo sapien |
| 40 | 120 | 10.7 | 233 | 2 | 08IX39 | 08ix39 homo sapien |
| 41 | 115 | 10.2 | 222 | 2 | 08IX38 | 08ix38 homo sapien |
| 42 | 115 | 10.2 | 287 | 2 | 09D7B8 | 09d7b8 mus musculu |
| 43 | 113 | 10.0 | 215 | 1 | CIB2_RAT | P54900 rattus norv |
| 44 | 112 | 10.0 | 186 | 2 | 062861 | 062861 rattus norv |
| 45 | 112 | 10.0 | 287 | 2 | 06SJP9 | 06sjp9 mus musculu |

ALIGNMENTS

RESULT 1
CIB3_RAT ID CIB3_RAT STANDARD; PRT; 215 AA.
AC 09jko0;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-3 subunit precursor.
GN Name=Scn3b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND PROBABLE DISULFIDE BONDS.
RC TISSUE=Brain;
RX MEDLINE=2010948; Pubmed=10688874; DOI=10.1073/pnas.030362197;
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
RA Plincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;
RT "beta3: an additional auxiliary subunit of the voltage-sensitive
RT sodium channel that modulates channel gating with distinct kinetics";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).
RN [2]
RP SEQUENCE FROM N.A., CHARACTERIZATION, TISSUE SPECIFICITY, AND SUBUNIT.
RC STRAIN=Sprague-Dawley; TISSUE=Dorsal root ganglion;
RX MEDLINE=21919106; Pubmed=11922146; DOI=10.1006/mene.2001.1039;
RA Qu Y., Curtis R., Lawson D., Gilbride K., Ge P., Distefano P.S.,
RA Sliros-Santiago I., Catterall W.A., Scheuer T.;
RT "Differential modulation of sodium channel gating and persistent
RT sodium currents by the beta1, beta2, and beta3 subunits";
RL Mol. Cell. Neurosci. 18:570-580(2001).
RN [3]
RP INTERACTION WITH NEUROFASCIN.
RX MEDLINE=21363577; Pubmed=11470829; DOI=10.1083/jcb.200102086;
RA Redcliffe C.F., Westendorp R.E., Curtis R., Catterall W.A.;
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin
RT through their extracellular immunoglobulin-like domain";
RL J. Cell Biol. 154:427-434(2001).
RN [4]
RP FUNCTION: Modulates channel gating kinetics. Causes unique
RP persistent sodium currents. Inactivates the sodium channel opening
RP slower than the beta-1 subunit. Its association with neurofascin
RP may target the sodium channels to the nodes of Ranvier of
RP developing axons and retain these channels at the nodes in mature
RP myelinated axons.
RN [5]
RP SUBUNIT: The voltage-sensitive sodium channel consists of an ion
RP conducting pore forming alpha-subunit regulated by one or more
RP beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
RP noncovalently associated with alpha, while beta-2 is covalently
RP linked by disulfide bonds. Beta-1 or beta-3 subunits associate
RP with neurofascin.
RN [6]
RP SUBCELLULAR LOCATION: Type I membrane protein.
RP TISSUE SPECIFICITY: Expressed broadly in neurons in the central
RP and peripheral nervous systems, but not in glia and most
RP nonneuronal cells. Weak detection in lung and adrenal gland.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ243395; CAB76838.1; -;
 DR HSBP; AF378093; AAK55415.1; -;
 DR HSBP; P06907; INEU.
 DR InterPro: IPR007110; IG-1-like.
 DR Pfam: PF00047; IG: 1.
 DR PROSITE: PS00835; IG-LIKE; 1.
 KM Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
 Signal; Sodium channel; Transmembrane; Voltage-gated channel.
 FT SIGNAL 1 24
 FT CHAIN 25 215
 FT DOMAIN 25 159 Sodium channel beta-3 subunit.
 FT TRANSMEM 160 180 Extracellular (Potential).
 FT DOMAIN 181 215 Potential.
 FT DOMAIN 25 138 Cytoplasmic (Potential).
 FT DISULFID 26 48 Ig-like C2-type.
 FT DISULFID 45 120 Potential.
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 103 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 215 AA; 24799 MW; 056B488E5EAE5F4F CRC64;
 Query Match 100.0%; Score 1125; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1e-94; Indels 0; Gaps 0;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAFRLPLASLVLIYWRVCPVCEVSETEAVOQNPMLRCISCKREVEATTVV 60
 DB 1 MPAFRLPLASLVLIYWRVCPVCEVSETEAVOQNPMLRCISCKREVEATTVV 60
 QY 61 EMFYRPGGKDFLIYRNGHOEVSPFGRIQWNGSKDLOVSTVTVANTLNDGGLTTC 120
 DB 61 EMFYRPGGKDFLIYRNGHOEVSPFGRIQWNGSKDLOVSTVTVANTLNDGGLTTC 120
 QY 121 NVSRFEFEARHPFKYTRRLPLRVTEAGEDEFTSVSEIMMYILLVFTLWLFEMTYC 180
 DB 121 NVSRFEFEARHPFKYTRRLPLRVTEAGEDEFTSVSEIMMYILLVFTLWLFEMTYC 180
 QY 181 YRKVSKAEAAQENASDYLAIPSENKENSVPVEE 215
 DB 181 YRKVSKAEAAQENASDYLAIPSENKENSVPVEE 215
 RESULT 2
 CIB3_MOUSE STANDARD; PRT; 215 AA.
 AC Q8BHK2; Q91Z99; Created
 DT 29-MAR-2004 (Rel. 43; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Sodium channel beta-3 subunit precursor.
 GN Name=Scn3b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Chen C., Avery C., Kazen-Gillespie K., Isom L.L.;
 RT "Mouse brain and heart beta 3 sodium channel cDNA."
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBD databases.
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nixido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru I., Haegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarali R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbali L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godik A., Gough J.,
 RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenlie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravelis T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shmada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Atzawa K., Atakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.V., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marnissi K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalderon M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carlini P., Prange C.J.,
 RA Raha S.S., Loquejano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarate P.H.,
 RA Richards S., Morley D.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,
 RA Villalón D.K., Mizny J.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Nadeau A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Modulates channel gating kinetics. Causes unique
 CC persistent sodium currents. Inactivates the sodium channel opening
 CC slower than the beta-1 subunit. Its association with neurofascin
 CC may target the sodium channels to the nodes of Ranvier of
 CC developing axons (By similarity).
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 CC conducting pore forming alpha-subunit regulated by one or more
 CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
 CC noncovalently associated with alpha, while beta-2 is covalently
 CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate
 CC with neurofascin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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CC EMBL: AY049036; AAL07512.1; -
 CC EMBL: AK049747; BAC33901.1; -
 CC EMBL: AK076466; BAC36356.1; -
 CC EMBL: BC053919; AAH53919.1; -
 CC EMBL: BC058636; AAH58636.1; -
 CC HSSP: P06907; INEU.
 CC MGI: MGI:1918882; Scn3b.
 CC InterPro: IPR007110; IG-like.
 CC Pfam: PF00047; Ig_1.
 CC PROSITE: PS00835; IG-LIKE; 1.
 CC Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
 CC Signal; Sodium channel; Transmembrane; Voltage-gated channel.
 CC CHAIN 1 24 Potential.
 CC DOMAIN 25 215 Sodium channel beta-3 subunit.
 CC TRANSMEM 160 180 Extracellular (potential).
 CC DOMAIN 181 215 Potential.
 CC DISULFID 26 48 Cytoplasmic (potential).
 CC FT 45 120 Ig-like C2-type.
 CC CARBOHYD 95 95 Potential.
 CC CARBOHYD 109 109 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 113 113 N-linked (GlcNAc...) (potential).
 CC CARBOHYD 121 121 N-linked (GlcNAc...) (potential).
 CC SEQUENCE 215 AA; 24789 MW; 0E07B4704178A423 CRC64;

Query Match 99.3%; Score 1117; DB 1; Length 215;
 Best Local Similarity 99.5%; Pred. No. 5.4e-94;
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPANFLPLPLASIVLIYWRVCPVCEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60
 DB 1 MPANFLPLPLASIVLIYWRVCPVCEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60
 QY 61 EWFYREPGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSTIVLNTLNDGSLYTC 120
 DB 61 EWFYREPGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSTIVLNTLNDGSLYTC 120
 QY 121 NVSRREFFEHRRFVVTTRLPLRVTEEGEDFTSVSEIMTYLILVFLTMLFIEMTYC 180
 DB 121 NVSRREFFEHRRFVVTTRLPLRVTEEGEDFTSVSEIMTYLILVFLTMLFIEMTYC 180
 QY 181 YRKVSKAEKAEQENASDYLAIPSENKENSVPVPEE 215
 DB 181 YRKVSKAEKAEQENASDYLAIPSENKENSVPVPEE 215

RESULT 3
 ID 069203 PRELIMINARY; PRT; 268 AA.
 AC 069203;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DE KIAA1158 protein (Fragment).
 GN Name=KIAA1158;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraka S.,
 RA Suga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones

RT Randomly Sampled from Sixe-Fractionated Libraries.;

RL DNA Res. 11:205-218(2004).
 DR EMBL: AK173115; BAD3293.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; IG-LIKE.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; IG_1.
 DR SMART: SM00406; Ig_1.
 DR PROSITE: PS00835; IG-LIKE; 1.
 DR NON TER 1
 SQ SEQUENCE 268 AA; 30330 MW; 7A265D5DD2409F CRC64;

Query Match 99.3%; Score 1117; DB 2; Length 268;
 Best Local Similarity 99.5%; Pred. No. 6.9e-94;
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPANFLPLPLASIVLIYWRVCPVCEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 60
 DB 54 MPANFLPLPLASIVLIYWRVCPVCEVPSSETEAVQGNPMKRCISCMKREBEVATTVV 113
 QY 61 EWFYREPGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSTIVLNTLNDGSLYTC 120
 DB 114 EWFYREPGKDFLIYRNGHQEVESPFQGRLOMNGSKLDQVSTIVLNTLNDGSLYTC 173
 QY 121 NVSRREFFEHRRFVVTTRLPLRVTEEGEDFTSVSEIMTYLILVFLTMLFIEMTYC 180
 DB 174 NVSRREFFEHRRFVVTTRLPLRVTEEGEDFTSVSEIMTYLILVFLTMLFIEMTYC 233
 QY 181 YRKVSKAEKAEQENASDYLAIPSENKENSVPVPEE 215
 DB 234 YRKVSKAEKAEQENASDYLAIPSENKENSVPVPEE 268

RESULT 4
 ID CIB3 HUMAN STANDARD; PRT; 215 AA.
 AC G9NY72; O9UR2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel beta-3 subunit precursor.
 GN Name=SCN3B; Synonyms=KIAA1158;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;
 RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
 RA Plincock R.D., Higgs J., Richardson P.J., Mizuguchi K., Jackson A.P.;
 RT "Beta3: an additional auxiliary subunit of the voltage-sensitive
 RT sodium channel that modulates channel gating with distinct kinetics.,"
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amygdala;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gaassenhuber J., Glassl S.,
 RA Ansoerge W., Boecher M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Wewers H.-W., Oettermann B., Obermayer B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Pouetka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.,"
 RT Genome Res. 11:422-435(2001).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,

RA Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RL from size-fractionated cDNA libraries from human brain.";
DNA Res. 6:329-336(1999).
CC -I- FUNCTION: Modulates channel gating kinetics. Causes unique
CC persistent sodium currents. Inactivates the sodium channel opening
CC slower than the beta-1 subunit. Its association with neurofascin
CC may target the sodium channels to the nodes of Ranvier of
CC myelinated axons and retain these channels at the nodes in mature
CC myelinated axons (By similarity).
CC -I- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
CC noncovalently associated with alpha, while beta-2 is covalently
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate
CC with neurofascin (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL, AJ243396; CAB76825.1; -;
DR EMBL, AB033589; CAB66524.1; -;
DR EMBL, AB033584; BAA86472.1; ALT_INIT.
DR HSSP; P06907; INEU.
DR Genew; HGNC:20665; SCN3B.
DR H-invdb; HIX0010216; -;
DR MIM; 608214; -;
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005248; P:voltage-gated sodium channel activity; NAS.
DR GO; GO:0006814; P:sodium ion transport; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.
FT SIGNAL 1 22
FT CHAIN 23 215
FT DOMAIN 23 159
FT TRANSMEM 160 180
FT DOMAIN 181 215
FT DOMAIN 32 154
FT DISULFID 26 48
FT CARBOHYD 95 120
FT CARBOHYD 109 109
FT CARBOHYD 113 113
FT CARBOHYD 121 121
SQ SEQUENCE 215 AA; 24702 MW; 70F6C604E9E26662 CRC64;
Query Match 98.2%; Score 1105; DB 1; Length 215;
Best Local Similarity 98.1%; Pred. No. 6-8e-93;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215
|||||
RESULT 5
CIB3_MACFA STANDARD; PRT; 215 AA.
ID CIB3_MACFA
AC Q8HXJ7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel beta-3 subunit precursor (Q8OA-13657).
GN Name=SCN3B;
OS Macaca fascicularis (Craab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Medulla oblongata;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: Modulates channel gating kinetics. Causes unique
CC persistent sodium currents. Inactivates the sodium channel opening
CC slower than the beta-1 subunit. Its association with neurofascin
CC may target the sodium channels to the nodes of Ranvier of
CC myelinated axons and retain these channels at the nodes in mature
CC myelinated axons (By similarity).
CC -I- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
CC noncovalently associated with alpha, while beta-2 is covalently
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate
CC with neurofascin (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
DR EMBL, AB097521; BAC41746.1; -;
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.
FT SIGNAL 1 22
FT CHAIN 23 215
FT DOMAIN 23 159
FT TRANSMEM 160 180
FT DOMAIN 181 215
FT DOMAIN 24 138
FT DISULFID 26 48
FT CARBOHYD 95 120
FT CARBOHYD 109 109
FT CARBOHYD 113 113
FT CARBOHYD 121 121
SQ SEQUENCE 215 AA; 24702 MW; 25319D5ED21BACF CRC64;
Query Match 97.5%; Score 1097; DB 1; Length 215;
Best Local Similarity 97.2%; Pred. No. 3.6e-92;
Matches 209; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 MPAFNRLPLASVILYMWVCPVCEVSETEAVOQNMKRCISCMKREBEVATTV 60
 QY 61 EMFYRPEGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTITLVNTLNDGSLYTC 120
 Db 61 EMFYRPEGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTITLVNTLNDGSLYTC 120
 QY 121 NVSRFEFPEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITC 180
 Db 121 NVSRFEFPEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITC 180
 QY 181 YRKVSRAEBAOENASDYLAIPSENKENSVPVEE 215
 Db 181 YRKVSRAEBAOENASDYLAIPSENKENSVPVEE 215
 RESULT 6
 Q6DB47 PRELIMINARY; PRT; 215 AA.
 AC 06DE47;
 DT 25-OCT-2004 (TEMBLrel. 28, Created)
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Scn3b-p10v protein.
 GN Name=scn3b-p10v;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCB1_TaxID=8355;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN 12
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.D., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lottner N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzyvinksi M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 13
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC077295; AAH77295.1; -
 DR InterPro: IPR003599; IG-
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG-v.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 1.
 SQ SEQUENCE 215 AA; 24472 MW; 2AAB80E46DE0289 CRC64;
 Query Match 62.2%; Score 700; DB 2; Length 215;
 Best Local Similarity 61.9%; Pred. No. 7, 4e-56;
 Matches 133; Conservative 31; Mismatches 51; Indels 0; Gaps 0;
 QY 1 MPAFNRLPLASVILYMWVCPVCEVSETEAVOQNMKRCISCMKREBEVATTV 60
 Db 1 MAAMENIFWTDVSLFLMVFVCPVCEVQSGTEAKGEMTLCTSCMKREBEVATTV 60
 QY 61 EMFYRPEGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTITLVNTLNDGSLYTC 120
 Db 61 EMFYRPEGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTITLVNTLNDGSLYTC 120
 QY 121 NVSRFEFPEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITC 180
 Db 121 NVSRFEFPEHARFPVKTRILPLRVTEBAGEDFTSVSEIMYTLVFLTMLFIEMITC 180
 QY 181 YRKVSRAEBAOENASDYLAIPSENKENSVPVEE 215
 Db 181 YRKVSRAEBAOENASDYLAIPSENKENSVPVEE 215
 RESULT 7
 CIB1_RABBIT STANDARD; PRT; 218 AA.
 ID CIB1_RABBIT
 AC P53788;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 GN Name=SCN1B;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCB1_TaxID=9986;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Sciatic nerve;
 RX MEDLINE=96235151; PubMed=8666261; DOI=10.1016/0378-1119(95)00871-3;
 RA Belcher S.M., Howe J.R.,
 RT "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
 RT rabbit";
 RL Gene 170:285-286(1996).
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional
 CC modulation of the heterotrimeric complex of the sodium channel.
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms
 CC from brain, skeletal muscle, and heart. Its association with
 CC neurofascin may target the sodium channels to the nodes of Ranvier
 CC of developing axons and retain these channels at the nodes in
 CC mature myelinated axons (By similarity).
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 CC conducting pore forming alpha-subunit regulated by one or more
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
 CC associated with alpha, while beta-2 is covalently linked by
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with
 CC neurofascin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: U35382; AB017572.1; -
 DR PIR: J04788; J04788.
 DR InterPro: IPR007110; IG-like.
 DR Pfam: PF00047; IG; 1.

DR PROSITE; PS50835; IG-LIKE; FALSE NEG.
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
 KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.
 FT SIGNAL 1 18
 FT CHAIN 19 218
 FT DOMAIN 19 160
 FT TRANSMEM 161 182
 FT DOMAIN 183 218
 FT DOMAIN 22 150
 FT DISULFID 21 43
 FT DISULFID 40 121
 FT CARBOHYD 93 93
 FT CARBOHYD 110 110
 FT CARBOHYD 114 114
 FT CARBOHYD 135 135
 SQ SEQUENCE 218 AA; 24706 MW; 39BD174E1FAEF7D2 CRC64;
 Query Match 41.8%; Score 470.5; DB 1; Length 218;
 Best Local Similarity 49.3%; Pred. No. 7.3e-35;
 Matches 105; Conservative 29; Mismatches 64; Indels 15; Gaps 6;
 QY 6 RLPLV---ASVLYIVWVRCFVCEVSETEAVGQGNPKKLCISCKMKEEVEATTVEW 62
 DB 3 RLALVVGALVSSAW-----GCVEVDSLETAVTGMTFKLICISCKRSETTAEFTBW 57
 QY 63 FYRPGGKDFL-IVEYRNGHQEVESP--FOGRLQWNGS---KDLQDVSTIVLNTLNDSG 116
 DB 58 TFRQGTETFEFKILTYENEVLQLEDEREGRVWVNGSGRTDLDLSFINTVNYNSG 117
 QY 117 LYTGVSEFEFEFENRPFVKTTRLIPRYTEBAGDFPSVSEIMYIIVLTMLPLE 176
 DB 118 DYQCHVYRLSPENYEHTNSVVKKIHLEVDKANDMDMSIVSEIMYIIVLTMLVAE 177
 QY 177 MYCYRKVSKA-EBAAGNADSYLAIPSENKEN 208
 DB 178 MYCYKTIATATEAAGNADSYLAIPSENKEN 210
 RESULT 8
 CIB1_HUMAN STANDARD; PRT; 218 AA.
 AC 007659;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 GN Name=SCN1B;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=93357746; PubMed=8394762;
 RA McClatchey A.L., Cannon S.C., Slaugenhaupt S.A., Gusella J.F.;
 RT "The cloning and expression of a sodium channel beta 1-subunit cDNA
 from human brain";
 RL Hum. Mol. Genet. 2:745-749(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart, and Skeletal muscle;
 RC MEDLINE=94171787; PubMed=8125980;
 RA Makita N., Bennett P.B. Jr., George A.L. Jr.;
 RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult
 human skeletal muscle, heart, and brain is encoded by a single gene";
 RL J. Biol. Chem. 269:7571-7578(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RC MEDLINE=95154833; PubMed=7851891;
 RA Makita N., Sloan-Brown K., Wegnulis D.O., Ropers H.-H.,
 RA George A.L. Jr.;

RT "Genomic organization and chromosomal assignment of the human voltage-
 gated Na+ channel beta 1 subunit gene (SCN1B).";
 RL Genomics 23:628-634(1994).
 RP VARIANT GFS+ TRP-121.
 RX MEDLINE=98361163; PubMed=9697698; DOI=10.1038/1252;
 RA Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr.,
 RA Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R.,
 RA Berkovic S.F., Mulley J.C.;
 RT "Febrile seizures and generalized epilepsy associated with a mutation
 in the Na(+)-channel beta-1 subunit gene SCN1B";
 RL Nat. Genet. 19:366-370(1998).
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional
 modulation of the heterotrimeric complex of the sodium channel.
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms
 from brain, skeletal muscle, and heart. Its association with
 neurofascin may target the sodium channels to the nodes of Ranvier
 or developing axons and retain these channels at the nodes in
 mature myelinated axons.
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 conducting pore forming alpha-subunit regulated by one or more
 beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
 associated with alpha, while beta-2 is covalently linked by
 disulfide bonds. Beta-1 or beta-3 subunits associate with
 neurofascin.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, heart
 and brain.
 CC -1- DISEASE: Defects in SCN1B are a cause of generalized epilepsy with
 febrile seizures plus (GFS+) [MIM:604233]. GFS+ is a disease
 characterized by a highly variable phenotype combining febrile
 seizures, generalized seizures often precipitated by fever at age
 6 years or more, and partial seizures, with a variable degree of
 severity.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; L10338; AAA60391.1; -;
 CC EMBL; L16242; AAA61277.1; -;
 CC EMBL; U12193; AAB97608.1; -;
 CC EMBL; U12189; AAB97608.1; JOINED.
 CC EMBL; U12190; AAB97608.1; JOINED.
 CC EMBL; U12191; AAB97608.1; JOINED.
 CC EMBL; U12192; AAB97608.1; JOINED.
 CC PIR; A55734; A55734.
 CC GeneW; HGNC:10586; SCN1B.
 CC MIM; 600235; -;
 CC GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
 CC GO; GO:0006814; P:sodium ion transport; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR007110; Ig-like.
 DR Pfam; PF000477; Ig-1.
 DR PROSITE; PS50835; IG-LIKE; FALSE NEG.
 KW Disease mutation; Epilepsy; Glycoprotein; Immunoglobulin domain;
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT SIGNAL 1 18
 FT CHAIN 19 218
 FT DOMAIN 19 160
 FT TRANSMEM 161 182
 FT DOMAIN 183 218
 FT DOMAIN 22 150
 FT DISULFID 21 43
 FT DISULFID 40 121
 FT CARBOHYD 93 93
 Potential.
 Sodium channel beta-1 subunit.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 Ig-like C2-type.
 Potential.
 Potential.
 N-linked (GlcNAc. . .) (Potential).

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FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT VARIANT 121 121 C->W (in GERS+).
SQ SEQUENCE 218 AA; 24707 MW; 09B812FA3F9E9018 CRC64;
Query Match 41.5%; Score 466.5; DB 1; Length 218;
Best Local Similarity 51.6%; Pred. No. 1.7e-34;
Matches 98; Conservative 26; Mismatches 57; Indels 7; Gaps 4;
QY 26 CVEPSETEAVQGNPKLRICSCMKREVEATVWVFYRPEGKDFL-ITYEYRNGHOEV 84
DB 21 CVEVDSETEAVVGMFTFKILICISCRSRETTAEFTETWTFQKTEEFVKILRYENEVLQ 80
QY 85 ESP--FQGRLOMNGS---KDLQDVSTIVLVNTLDSGLTYCNVSRPEFEAHNPFPVKTTR 139
DB 81 EEDEREFGKRVVWNGSGRTKDLQDLSIFITVTVNHSQDYCHYVRLFFPNYEHTSVVK 140
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILVFLTLFEMICYRKVSKA-EEAQAENASDY 198
DB 141 KIHLEVDKRNDRMASIVSEIMMYILVFLTLVLAEMICYKKAAPATTAQAENASEY 200
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
RESULT 9
CIB1_RAT STANDARD; PRT; 218 AA.
ID CIB1_RAT
AC 000954;
DT 01-JUL-1993 (Rel. 26, Last Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN Name=Scn1b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN 1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92271207; PubMed=1375395.
RA Isom L.V., De Jongh K.S., Patton D.E., Reber B.F.X., Offord J.,
RA Charbonneau H., Walsh K., Goldin A.L., Catterall W.A.;
RT "Primary structure and functional expression of the beta 1 subunit of
RT the rat brain sodium channel.";
RL Science 256:839-842 (1992).
RN 2)
RP INTERACTION WITH NEUROFASCIN.
RA MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;
RA Rattcliffe C.F., Westbroek R.E., Curtis R., Catterall W.A.;
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin
RT through their extracellular immunoglobulin-like domain.";
RL J. Cell Biol. 154:427-434 (2001).
CC -1- FUNCTION: Crucial in the assembly, expression, and functional
CC modulation of the heterotrimeric complex of the sodium channel.
CC The beta-1 subunit can modulate multiple alpha subunit isoforms
CC from brain, skeletal muscle, and heart. Its association with
CC neurofascin may target the sodium channels to the nodes of Ranvier
CC of developing axons and retain these channels at the nodes in
CC mature myelinated axons.
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
CC associated with alpha, while beta-2 is covalently linked by
CC disulfide bonds. Beta-1 or beta-3 subunits associate with
CC neurofascin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, heart, skeletal muscle and
CC spinal cord.

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CC -1- DEVELOPMENTAL STAGE: In developing nodes of Ranvier, it is
CC localized in the sciatic nerve at postnatal days 3 and 10, during
CC the process of myelination and maturation of the nodes.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC *****
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M91808; AAA88513.1; -.
DR PIR: A42737; A42737.
DR RGD: 3631; Scn1b.
DR InterPro: IPR007110; Ig_1-like.
DR Pfam: PF00047; Ig_1.
DR PROSITE: PS50835; IG LIKE; FALSE NEG.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT SIGNAL 1 18
FT CHAIN 19 218 Sodium channel beta-1 subunit.
FT DOMAIN 19 160 Extracellular (Potential).
FT TRANSMEM 161 182 Potential.
FT DOMAIN 183 218 Cytoplasmic (Potential).
FT DOMAIN 22 150 Ig-1-like C2-type.
FT DISULFID 21 43 Potential.
FT DISULFID 40 121 Potential.
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 218 AA; 24692 MW; 0BA84FC44FE2306B CRC64;
Query Match 41.2%; Score 463.5; DB 1; Length 218;
Best Local Similarity 51.1%; Pred. No. 3.2e-34;
Matches 97; Conservative 29; Mismatches 57; Indels 7; Gaps 4;
QY 26 CVEPSETEAVQGNPKLRICSCMKREVEATVWVFYRPEGKDFL-ITYEYRNGHOEV 84
DB 21 CVEVDSETEAVVGMFTFKILICISCRSRETTAEFTETWTFQKTEEFVKILRYENEVLQ 80
QY 85 ESP--FQGRLOMNGS---KDLQDVSTIVLVNTLDSGLTYCNVSRPEFEAHNPFPVKTTR 139
DB 81 EEDEREFGKRVVWNGSGRTKDLQDLSIFITVTVNHSQDYCHYVRLFFPNYEHTSVVK 140
QY 140 LIPLRVTEAGEDEFTSVSEIMMYILVFLTLFEMICYRKVSKA-EEAQAENASDY 198
DB 141 KIHLEVDKRNDRMASIVSEIMMYILVFLTLVLAEMICYKKAAPATTAQAENASEY 200
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
QY 199 LAIPSENKEN 208
DB 201 LAITSESKEN 210
RESULT 10
CIB1_MOUSE STANDARD; PRT; 218 AA.
ID CIB1_MOUSE
AC P97952;
DT 15-JUL-1998 (Rel. 36, Last Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN Name=Scn1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1)
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Brain;

```


RX MEDLINE=97165884; PubMed=9013777; DOI=10.1016/S0169-328X(96)00123-4;
 RA Grosen C.L.S., Cannon S.C., Corey D.P., Gussella J.F.;
 RT "Sequence of the voltage-gated sodium channel beta1-subunit in wild-
 RT type and in quivering mice";
 RL Brain Res. Mol. Brain Res. 42:222-226(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98387156; PubMed=9721701;
 RA Kupersmidt S., Yang T., Roden D.M.;
 RT "Modulation of cardiac Na⁺ current phenotype by beta1-subunit
 RT expression";
 RL Circ. Res. 83:441-447(1998).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.T., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional
 CC modulation of the heterotrimeric complex of the sodium channel.
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms
 CC from brain, skeletal muscle, and heart. Its association with
 CC neurofascin may target the sodium channels at the nodes of Ranvier
 CC of developing axons and retain these channels at the nodes in
 CC mature myelinated axons (By similarity).
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 CC conducting pore forming alpha-subunit regulated by one or more
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
 CC associated with alpha, while beta-2 is covalently linked by
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with
 CC neurofascin (By similarity).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC
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 CC
 CC -----
 CC EMBL; U46681; AAC53006.1; -;
 DR EMBL; U85786; AAB49368.1; -;
 DR EMBL; BC009652; AAH09652.1; -;
 DR EMBL; BC039140; AAH39140.1; -;
 DR MGD; MGI:98247; Scn1b.
 DR InterPro; IPR007110; I9-1ike.
 DR Pfam; PF00047; I9; 1.
 DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
 KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.
 FT SIGNAL 1 18 By similarity.
 FT CHAIN 19 218 Sodium channel beta-1 subunit.
 FT DOMAIN 19 160 Extracellular (Potential).

FT TRANSMEM 161 182 Potential.
 FT DOMAIN 183 218 Cytoplasmic (Potential).
 FT SIGNAL 22 150 Ig-like C2-type.
 FT DISULFID 21 43 Potential.
 FT DISULFID 40 121 Potential.
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 218 AA; 24650 MW; 5198F3383B0A8C45 CRC64;
 Query Match 41.0%; Score 461; DB 1; Length 218;
 Best Local Similarity 48.8%; Pred. No. 5,4e-34;
 Matches 100; Conservative 31; Mismatches 62; Indels 12; Gaps 5;
 QY 11 ASVLIVYVRCFPCVCEVPSETEAVQGNPMKLCISGMKEEYATVWPFRECKG 70
 DB 11 AALVSSAW-----GCGVEVDSDTEAVYGMTFKILCISCKRSEYTAETFTWTRQKTE 65
 QY 71 DFLIYEVYRNGHOVEESP--FQGRLOWNGS--XDLQVSTIVLVNTLNDGLYTCVNSR 124
 DB 66 EFVKIRKRENEVLQLEDEDEREGRVVWNGSGTDLQDLSIFITNVYVNHSGDYECVHYR 125
 QY 125 EEEFPAHPEVKTTRLPLRVTEBAGDEFTSVSEIMMYIILVFLTMLFTEMTCRKV 184
 DB 126 LLFEDNYEHNTSVVVKIHLFEVDKRNDRMADISVEIMMYVILVILVLAEMVYCYKXI 185
 QY 185 SKA--EAAQENASDYLAIPSENKEN 208
 DB 186 AATETAAQENASEYLAITSEKEN 210
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 AC Q8WU42;
 DT 01-MAR-2002 (TRENBLREL, 20, Created)
 DT 01-MAR-2004 (TRENBLREL, 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL, 26, Last annotation update)
 DE SCN1B protein (Fragment).
 GN Name=SCN1B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.T., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;

Job time : 118 secs

RX MEDLINE=95024086; PubMed=7937931;
RA Oh Y., Waxman S.G.;
RT "The beta 1 subunit mRNA of the rat brain Na⁺ channel is expressed in
RT glial cells";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9985-9989(1994).
DR EMBL; L48688; AAB02428.1; -;
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER
SQ SEQUENCE 66 AA; 7208 MW; 4DB598740914D95B CRC64;

Query Match 18.2%; Score 204.5; DB 2; Length 66;
Best Local Similarity 67.2%; Pred. No. 4e-11;
Matches 39; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 152 DFTSVSEIMMYLIVFLTWLFIEMICYRVSKA-EAAQENASDYLAIPSENKEN 208
DB 1 DMASTVSEIMMYLIVFLTWLVAEMVVCYKKAATAEAQENASEYLAITSSEKEN 58

RESULT 15

08JFG6 PRELIMINARY; PRT; 203 AA.
AC 08JFG6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Myelin protein zero.
GN Name=mpz;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myelin;
RA Schwelltzer J., Becker T., Becker C.G., Schachner M.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ489219; CAD32961.1; -;
DR HSSP; P06907; INEU.
DR ZFIN; ZDB-GENE-010724-4; mpz.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000920; Myelin_PO.
DR PRINTS; PR00213; MYELINPO.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 203 AA; 22097 MW; 12614E9076D373D1 CRC64;

Query Match 15.6%; Score 175.5; DB 2; Length 203;

Best Local Similarity 26.5%; Pred. No. 6.4e-08;
Matches 53; Conservative 41; Mismatches 89; Indels 17; Gaps 7;

QY 7 LLPLASLVLIYVWRCFPVCVEVPSETEAVQGNPKLRICISCMKREVEATTVVEMFYRP 66
DB 4 VLALTSVVLIGTASQSTLAVVTDSKHALVGSVDRLGC-SFSSMQWTSPEVSPFTWHYRP 62
QY 67 EGGRKDFL-IYERYNG--HOEVESPFQGRLOMNGSKDLODVSTIVNTLNDGLTCNVIS 123
DB 63 DGAKDAISIFHYGGGEAVPANKGFQNRLEFVGNPSRDSILIKNLDGNGTPTCDAK 122
QY 124 REFEEARHPFKTRRLPL-RVTEAGBDFTSVSEIMMYLIV---FLTWLFIEMI 178
DB 123 NPPDIGH--PSTRLLVFERKVPVQAGVTGSTITGVNLILVAIYILMRFLVARRV 179
QY 179 YC----YRKVSKAEAAQE 193
DB 180 FSLSMKHKGKKGKSGSQ 199

Search completed: March 31, 2005, 20:21:49

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:01:32 ; Search time 124.5 Seconds
(without alignments)
667.899 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLYWVS.....SDYLAIPEKENSAPVVEE 215

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1124 | 100.0 | 215 | 3 | AAB36002 Human bet |
| 2 | 1124 | 100.0 | 215 | 4 | AAB85206 Human nov |
| 3 | 1124 | 100.0 | 215 | 5 | ABBO5689 Human sig |
| 4 | 1124 | 100.0 | 215 | 6 | AAB35366 Human sod |
| 5 | 1124 | 100.0 | 215 | 7 | ABR83183 Human SCN |
| 6 | 1105 | 98.3 | 215 | 3 | AAB36001 Rat betas |
| 7 | 1105 | 98.3 | 215 | 4 | AAB50243 Rat sodiu |
| 8 | 1105 | 98.3 | 215 | 6 | AAB35367 Rat sodiu |
| 9 | 1024 | 91.1 | 195 | 4 | AAM79212 Human pro |
| 10 | 986 | 87.7 | 191 | 4 | AAB50245 Rat sodiu |
| 11 | 942.5 | 83.9 | 369 | 4 | ABG25577 Novel hum |
| 12 | 843 | 75.0 | 159 | 3 | AAB36020 Human bet |
| 13 | 834 | 74.2 | 157 | 8 | ADSI0835 Human the |
| 14 | 834 | 74.0 | 159 | 3 | AAB36021 Rat betas |
| 15 | 694 | 61.7 | 1176 | 4 | ABG22576 Novel hum |
| 16 | 477 | 42.4 | 218 | 4 | AAB50260 Rabbit so |
| 17 | 472 | 42.0 | 218 | 3 | AAB36031 Rat betai |
| 18 | 472 | 42.0 | 218 | 4 | AAB62326 Rat sodiu |
| 19 | 471 | 41.9 | 218 | 6 | ABBR8771 Human vol |
| 20 | 471 | 41.9 | 218 | 7 | AAB35363 Human sod |
| 21 | 471 | 41.9 | 218 | 8 | ABR83181 Human SCN |
| 22 | 471 | 41.9 | 218 | 8 | ADQ67223 Human vol |
| 23 | 471 | 41.8 | 218 | 7 | ADQ19429 Human sof |
| 24 | 470 | 41.8 | 218 | 7 | ADB78601 Human sod |
| 25 | 463 | 41.2 | 218 | 7 | ADB78602 Human sod |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 408.5 | 36.3 | 206 | 4 | ABG22575 Novel hum |
| 27 | 258.5 | 23.0 | 268 | 5 | AAB36034 Human bet |
| 28 | 245 | 21.9 | 272 | 4 | AAB62320 Rat sodiu |
| 29 | 246 | 21.9 | 272 | 4 | AAB20371 Sodium ch |
| 30 | 234 | 20.8 | 74 | 4 | ABBI1698 Human vol |
| 31 | 234 | 20.8 | 74 | 4 | AAB60196 Human pro |
| 32 | 207 | 18.4 | 39 | 3 | AAB36015 Human bet |
| 33 | 196 | 17.4 | 39 | 3 | AAB36016 Rat betas |
| 34 | 175 | 15.6 | 248 | 7 | ADSE6862 Rat prote |
| 35 | 167 | 14.9 | 248 | 6 | ABM04838 Rat schwa |
| 36 | 165 | 14.7 | 34 | 3 | AAB36029 Human bet |
| 37 | 163.5 | 14.5 | 258 | 5 | AAM52696 Human mye |
| 38 | 161 | 14.3 | 34 | 3 | AAB36034 Rat betas |
| 39 | 160.5 | 14.3 | 235 | 4 | AAV72879 Human PRO |
| 40 | 160.5 | 14.3 | 235 | 5 | AAU83710 Human PRO |
| 41 | 160.5 | 14.3 | 235 | 6 | ABU80857 Human PRO |
| 42 | 160.5 | 14.3 | 235 | 6 | ABO33823 Novel hum |
| 43 | 160.5 | 14.3 | 235 | 6 | ABG74763 Human PRO |
| 44 | 160.5 | 14.3 | 235 | 6 | ABU82166 Novel hum |
| 45 | 160.5 | 14.3 | 235 | 6 | ABU82166 Novel hum |

ALIGNMENTS

RESULT 1
AAB36002 standard, protein; 215 AA.

ID AAB36002;

DE 15-FEB-2001 (first entry)

XX Human betas3 subunit.

XX Human, beta sub-unit; betas3; analgesic; anticonvulsant;

KW cerebroprotective; vasotropic; cardiant; nootropic; cytosolic;

KW dermatological; gene therapy; voltage-gated sodium channel; pain;

KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;

XX Charcot Marie Tooth disease.

XX Homo sapiens.

XX WO20006367-A1.

XX 24-FEB-2000; 2000WO-EP001783.

XX 15-APR-1999; 99US-0129473P.

XX (WARN) WARNER LAMBERT CO.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

XX WPI, 2000-665241/64.

XX N-PSDB; AAC67837.

PT Novel nucleic acid encoding a beta-3 subunit from a voltage-gated sodium

PT channel, and their corresponding polypeptides, useful for detecting and

PT treating sodium channel-associated conditions, e.g. pain, epilepsy and

XX Claim 34; Fig 4; 88pp; English.

XX The present sequence is given in the claims of a specification relating

XX to a novel family of beta sub-unit proteins from a voltage-gated sodium

XX channel. Human and rat beta sub-units, which have been collectively

XX identified as betas, have been isolated. The polynucleotides and

XX polypeptides are useful for screening for agonists and antagonists of

XX sodium channels. The agonists, antagonists, proteins and nucleic acids

CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX

XX Sequence 215 AA;

Query Match . . . 100.0%; Score 1124; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPMKLRICSCMKKEEVEATTIV 60
DB 1 MPAFRLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPMKLRICSCMKKEEVEATTIV 60
QY 61 EMFYRPEGKDFLITYEYNGHGVESPPQGRLOMNGSKDLDVSTIVNTVLTNDGSLTTC 120
DB 61 EMFYRPEGKDFLITYEYNGHGVESPPQGRLOMNGSKDLDVSTIVNTVLTNDGSLTTC 120
QY 121 NVSRFEFEARHPFVKTRRLPLRVTBEAGDEFTSVSEIMMYILLVFLTLMLEMTYC 180
DB 121 NVSRFEFEARHPFVKTRRLPLRVTBEAGDEFTSVSEIMMYILLVFLTLMLEMTYC 180
QY 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215
DB 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215

RESULT 2

ABB85206
ID AAB85206 standard; protein; 215 AA.

XX AAB85206;

XX 07-SEP-2001 (first entry)

DE Human novel sodium channel beta1-like subunit.

XX Sodium channel; sensory neurone specific channel; beta1-like subunit;

KW SNS; therapeutic; pain; analgesic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 38..122 /note="immunoglobulin domain"

XX Domain 157..176 /note="transmembrane domain"

XX MO200144293-A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 2000WO-GB004802.

XX 17-DEC-1999; 99GB-00029970.

XX (GLAXO) GLAXO GROUP LTD.

XX Plumpton M, Powell AJ, Sauseau P;

XX WPI; 2001-398129/42.

XX N-PSDB; AAF84146.

XX Novel sub-unit for voltage-gated sodium channel proteins for producing

XX agents useful for treating pain.

XX Claim 1; Fig 2; 31pp; English.

CC The invention provides a novel beta1-like sub-unit for voltage-gated
CC sodium ion channel polypeptide, specifically a sensory neurone specific
CC channel (SNS) subunit. The novel beta1-like subunit is useful for
CC producing a therapeutic agent which is useful treating pain in a patient.

CC The subunit can be expressed by standard recombinant methodology. The
CC present sequence represents a human novel sodium channel beta1-like
CC subunit
XX

XX Sequence 215 AA;

Query Match . . . 100.0%; Score 1124; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPMKLRICSCMKKEEVEATTIV 60
DB 1 MPAFRLPLASLVLIYVWSVCFPVCEVPSSETEAQGNPMKLRICSCMKKEEVEATTIV 60
QY 61 EMFYRPEGKDFLITYEYNGHGVESPPQGRLOMNGSKDLDVSTIVNTVLTNDGSLTTC 120
DB 61 EMFYRPEGKDFLITYEYNGHGVESPPQGRLOMNGSKDLDVSTIVNTVLTNDGSLTTC 120
QY 121 NVSRFEFEARHPFVKTRRLPLRVTBEAGDEFTSVSEIMMYILLVFLTLMLEMTYC 180
DB 121 NVSRFEFEARHPFVKTRRLPLRVTBEAGDEFTSVSEIMMYILLVFLTLMLEMTYC 180
QY 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215
DB 181 YRKVSKAEBAQAQENASDYLAIPSENKENSAPVVEE 215

RESULT 3

ABB05689
ID ABB05689 standard; protein; 215 AA.

XX ABB05689;

XX 30-APR-2002 (first entry)

DE Human signal transduction protein clone amy2_2118.

XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;

KW gene therapy.

XX Homo sapiens.

XX WO200198454-A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-IB002050.

XX 25-APR-2000; 2000US-0199380P.

XX (GEHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2002-055860/07.

XX N-PSDB; ABA93727.

XX Human cDNA sequences and clones derived from human fetal brain, fetal

XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic

XX screening and therapy.

XX Claim 1; Page 176; 611pp; English.

CC The present invention describes assemblages and computer readable media
CC comprising novel human cDNA sequences and clones derived from human
CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
CC present invention which encode the proteins given in ABB05682 to
CC ABB05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in a variety of applications, for example
CC they may be used in profiling assays, for providing large arrays of human
CC genetic material for implementing large-scale screening strategies and
CC for treating diseases via gene therapy procedures

XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASIVLIYWSVCPVCVEPSETEAVQGNPKRCISCMKREBEATTV 60
DB 1 MPANRLPLASIVLIYWSVCPVCVEPSETEAVQGNPKRCISCMKREBEATTV 60
QY 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNSKDIQDVSITVLTNLSGLYTC 120
DB 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNSKDIQDVSITVLTNLSGLYTC 120
QY 121 NVSREFFEHARPPVKTRILPLRVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180
DB 121 NVSREFFEHARPPVKTRILPLRVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180
QY 181 YRKVSKAEAAQENASDYLAIPSENKNSAVPVEE 215
DB 181 YRKVSKAEAAQENASDYLAIPSENKNSAVPVEE 215

RESULT 4
AAE35366
ID AAE35366 standard; protein: 215 AA.

AC AAE35366;
DT 17-JUN-2003 (first entry)

DE Human sodium channel beta-3 subunit.

XX Human; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;
KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;
KM bipolar affective disorder; attention deficit disorder; phobic disorder;
KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;
KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;
KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;
KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;
KM bone metabolism disorder; endothelial cell disorder; viral encephalitis;
KM acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;
KM poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;
KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;
KM pain.

XX Homo sapiens.

XX Key Location/Qualifiers
XX Domain 38..70
XX /note= "Conserved motif"
XX Domain 104..122
XX /note= "Conserved motif"

XX EPI258495-A1.
XX 20-NOV-2002.
XX 09-MAY-2002; 2002BP-00253262.
XX 09-MAY-2001; 2001US-0289893P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Curtis Raj;

XX WPI; 2003-185859/19.

XX New isolated human sodium channel beta-4 subunit nucleic acid molecule
PT and polypeptide, useful for diagnosing and treating disorders with
PT aberrant beta-4 subunit function or expression, such as neurological and
PT cardiovascular diseases.

XX
PS Disclosure; Page 55-56; 62pp; English.

XX The invention relates to human sodium channel beta-4 subunit, 98359
CC polypeptides and polynucleotides. The methods and compositions of the
CC invention are useful for diagnosing, screening and treating disorders
CC associated with aberrant or deficient sodium channel beta-4 subunit
CC function or expression such as paroxysmal congenital, hyperkalemic
CC periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic
CC disorders, attention deficit disorder, obsessive-compulsive disorder and
CC bipolar affective disorder), dementia, cardiovascular disorders
CC (hypertension, shock, heart failure, arrhythmias and cardiomyopathy),
CC neurological disorders (Alzheimer's or Parkinson's disease,
CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders
CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone
CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,
CC herpes simplex, poliomyelitis, viral encephalitis and peripheral
CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple
CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's
CC disease and Leigh disease). Polynucleotides of the invention are used to
CC identify an individual from a biological sample (tissue typing), and in
CC forensic identification of a biological sample. The invention is useful
CC in gene therapy. The present sequence is human sodium channel beta-3
CC subunit. This sequence is used in the invention

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASIVLIYWSVCPVCVEPSETEAVQGNPKRCISCMKREBEATTV 60
DB 1 MPANRLPLASIVLIYWSVCPVCVEPSETEAVQGNPKRCISCMKREBEATTV 60
QY 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNSKDIQDVSITVLTNLSGLYTC 120
DB 61 EWFYRPGKDFLIYERNHQEVESPFQGRLOMNSKDIQDVSITVLTNLSGLYTC 120
QY 121 NVSREFFEHARPPVKTRILPLRVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180
DB 121 NVSREFFEHARPPVKTRILPLRVTEAGEDEFTSVSEIMMYTLVFTLMLIEMIYC 180
QY 181 YRKVSKAEAAQENASDYLAIPSENKNSAVPVEE 215
DB 181 YRKVSKAEAAQENASDYLAIPSENKNSAVPVEE 215

XX Homo sapiens.

XX Key Location/Qualifiers
XX Domain 38..70
XX /note= "Conserved motif"
XX Domain 104..122
XX /note= "Conserved motif"

XX EPI258495-A1.
XX 20-NOV-2002.
XX 09-MAY-2002; 2002BP-00253262.
XX 09-MAY-2001; 2001US-0289893P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Curtis Raj;

XX WPI; 2003-185859/19.

XX New isolated human sodium channel beta-4 subunit nucleic acid molecule
PT and polypeptide, useful for diagnosing and treating disorders with
PT aberrant beta-4 subunit function or expression, such as neurological and
PT cardiovascular diseases.

XX George AL, Lossin C;
 XX
 XX WPI: 2003-712725/67.
 DR N-PSDB; ACF57870.
 XX
 XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 PT screening for modulators, for treating e.g. epilepsy.
 PT
 PS Disclosure; Page 145-147, 176pp; English.
 XX
 XX The invention relates to a recombinantly expressed and isolated human
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
 CC incorporated into a cell, is used to screen for specific modulators,
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 CC motor endplate diseases, hypertension, congestive heart failure and
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 CC and metastatic cancer cell lines). These activities can also be provided
 CC by gene therapy vectors that express (I) or the modulators. The
 CC modulators, also antibodies directed against (I), are used to detect
 CC sodium channel polypeptides. The present sequence represents a human
 CC SCN1B protein
 CC
 SQ Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 7; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.4e-98;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIIVWVSCFPCVCEVSETEAVQGNPKMLRCISCMKREVEATTIV 60
 DB 1 MPAFRLPLASLVIIVWVSCFPCVCEVSETEAVQGNPKMLRCISCMKREVEATTIV 60
 QY 61 EMFYRPEGGKDLIYENRNGHOEVESPPQGRLONNGSKDLOVSTIVLVNTLNDGGLTTC 120
 DB 61 EMFYRPEGGKDLIYENRNGHOEVESPPQGRLONNGSKDLOVSTIVLVNTLNDGGLTTC 120
 QY 121 NVSRFEFEARHPFYKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLIEMTIC 180
 DB 121 NVSRFEFEARHPFYKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLIEMTIC 180
 QY 181 YRKVSKAEAAQENASDYLAIPESENKENSAPVEE 215
 DB 181 YRKVSKAEAAQENASDYLAIPESENKENSAPVEE 215

RESULT 6

AAB36001
 ID AAB36001 standard; protein; 215 AA.

AC AAB36001;

DT 15-FEB-2001 (first entry)

DE Rat beta3 subunit.

XX Rat, beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
 XX vasotrophic; cardiac; nootropic; cytostatic; dermatological;
 XX gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
 XX ischaemia; heart disease; Jacobsen Syndrome;
 XX familial nonchromaffin paraganglioma; phenylketonuria;
 XX Charcot Marie Tooth disease.

OS Rattus sp.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.
 XX (WARN) WARNER LAMBERT CO.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 XX Cox P, Dixon A, Jackson A, Morgan K;
 PI WPI: 2000-665241/64.
 DR N-PSDB; AAC67836.
 XX
 XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
 PT channel, and their corresponding polypeptides, useful for detecting and
 PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
 PT stroke.
 PS Claim 33; Fig 4; 88pp; English.
 XX
 XX The present sequence is given in the claims of a specification relating
 CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
 CC channel. Human and rat beta sub-units, which have been collectively
 CC identified as beta3, have been isolated. The polynucleotides and
 CC polypeptides are useful for screening for agonists and antagonists of
 CC sodium channels. The agonists, antagonists, proteins and nucleic acids
 CC may be used diagnosing of treating diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
 CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
 CC Phenylketonuria and Charcot Marie Tooth disease
 CC
 SQ Sequence 215 AA;

Query Match 98.3%; Score 1105; DB 3; Length 215;
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;

Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVIIVWVSCFPCVCEVSETEAVQGNPKMLRCISCMKREVEATTIV 60
 DB 1 MPAFRLPLASLVIIVWVSCFPCVCEVSETEAVQGNPKMLRCISCMKREVEATTIV 60
 QY 61 EMFYRPEGGKDLIYENRNGHOEVESPPQGRLONNGSKDLOVSTIVLVNTLNDGGLTTC 120
 DB 61 EMFYRPEGGKDLIYENRNGHOEVESPPQGRLONNGSKDLOVSTIVLVNTLNDGGLTTC 120
 QY 121 NVSRFEFEARHPFYKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLIEMTIC 180
 DB 121 NVSRFEFEARHPFYKTRRLIPLRVTEBAGEDFTSVSEIMMYILLVFLTMLIEMTIC 180
 QY 181 YRKVSKAEAAQENASDYLAIPESENKENSAPVEE 215
 DB 181 YRKVSKAEAAQENASDYLAIPESENKENSAPVEE 215

RESULT 7

AAB50243
 ID AAB50243 standard; protein; 215 AA.

AC AAB50243;

DT 13-MAR-2001 (first entry)

DE Rat sodium channel beta3 protein Alrx94h5.

XX Rat, sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
 XX neurodegenerative disorder; mood disorder; muscle contraction.

OS Rattus sp.

PN WO200069912-A1.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US013144.

PR 14-MAY-1999; 99US-0134198P.

XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAD;
 PI WPI, 2001-122743/13.
 DR N-PSDB; AAC90600.
 XX
 XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.
 XX
 XX Claim 9; Fig 2; 145bp; English.
 XX
 XX The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta-3 protein, designated Altra945. This protein is
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics
 XX
 XX Sequence 215 AA;
 SQ
 Query Match 98.3%; Score 1105; DB 4; Length 215;
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;
 Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MPANRLPLASIVLIVYVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTVV 60
 Db 1 MPANRLPLASIVLIVYVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTVV 60
 QY 61 EWFYRGGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
 Db 61 EWFYRGGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
 QY 121 NVSRREFEFAHNPFTVTRLLIPRVTEEGEDFTSVSSIMYILLVFLTMLIEMITC 180
 Db 121 NVSRREFEFAHNPFTVTRLLIPRVTEEGEDFTSVSSIMYILLVFLTMLIEMITC 180
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215
 Db 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215
 RESULT 8
 ID AAE35367 standard; protein; 215 AA.
 XX
 XX AAE35367;
 AC
 XX 17-JUN-2003 (first entry)
 DT
 XX
 XX Rat sodium channel beta-3 subunit.
 DE
 XX
 XX Rat; sodium channel beta-3 subunit; 98359 protein; gene therapy; AIDS;
 KM shock; hypertension; psychiatric disease; obsessive-compulsive disorder;
 KM bipolar affective disorder; attention deficit disorder; phobic disorder;
 KM cardiovascular disorder; neurological disorder; spinocerebellar ataxia;
 KM Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;
 KM autoimmune disorder; cellular proliferative disorder; Krabbe's disease;
 KM metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;
 KM bone metabolism disorder; endothelial cell disorder; viral encephalitis;
 KM acquired immune deficiency syndrome; peripheral neuropathy; arhythmia;
 KM polioomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;
 KM dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;
 KM pain.
 KM
 XX Rattus norvegicus.
 OS
 XX Key Location/Qualifiers
 FH Domain 68.. 64
 FT

PT /note="Conserved motif"
 FT Domain 104..122
 FT 104..122 /note="Conserved motif"
 XX
 XX EPI258495-A1.
 XX
 XX 20-NOV-2002.
 XX
 XX 09-MAY-2002; 2002EP-00253262.
 PF 09-MAY-2001; 2001US-0289893P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAD;
 PI WPI, 2003-185859/19.
 DR
 XX
 XX New isolated human sodium channel beta-4 subunit nucleic acid molecule
 PT and polypeptide, useful for diagnosing and treating disorders with
 PT aberrant beta-4 subunit function or expression, such as neurological and
 PT cardiovascular diseases.
 XX
 XX Disclosure; Page 56; 62pp; English.
 XX
 XX The invention relates to human sodium channel beta-4 subunit, 98359
 CC polypeptides and polynucleotides. The methods and compositions of the
 CC invention are useful for diagnosing, screening and treating disorders
 CC associated with aberrant or deficient sodium channel beta-4 subunit
 CC function or expression such as paramyotonia congenital, hyperalaemic
 CC periodic paralysis, epilepsy, psychiatric diseases (anxiety or phobic
 CC disorders, attention deficit disorder, obsessive-compulsive disorder and
 CC bipolar affective disorder), dementia, cardiovascular disorders
 CC (hypertension, shock, heart failure, arhythmias and cardiomyopathy),
 CC neurological disorders (Alzheimer's or Parkinson's disease,
 CC spinocerebellar ataxia and Tourette's syndrome), autoimmune disorders
 CC (diabetes, arthritis), cellular proliferative disorders (cancer), bone
 CC metabolism disorders, liver disorders, viral infections (AIDS, rabies,
 CC herpes simplex, poliomyelitis, viral encephalitis and peripheral
 CC neuropathy), endothelial cell disorders, demyelinating diseases (multiple
 CC sclerosis), pain and/or metabolic disorders (leukodystrophies, Krabbe's
 CC disease and Leigh disease). Polynucleotides of the invention are used to
 CC identify an individual from a biological sample (tissue typing), and in
 CC forensic identification of a biological sample. The invention is useful
 CC in gene therapy. The present sequence is rat sodium channel beta-3
 CC subunit. This sequence is used in the invention
 CC
 XX
 XX Sequence 215 AA;
 SQ
 Query Match 98.3%; Score 1105; DB 6; Length 215;
 Best Local Similarity 98.1%; Pred. No. 1.5e-96;
 Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MPANRLPLASIVLIVYVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTVV 60
 Db 1 MPANRLPLASIVLIVYVCPVCEVPSSETEAVQGNPMKLRCSCKMREVEATTVV 60
 QY 61 EWFYRGGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
 Db 61 EWFYRGGKDFLIYERNHGVESPPQGRLOMNSKDLQDVSTIVLNTLNDGSLYTC 120
 QY 121 NVSRREFEFAHNPFTVTRLLIPRVTEEGEDFTSVSSIMYILLVFLTMLIEMITC 180
 Db 121 NVSRREFEFAHNPFTVTRLLIPRVTEEGEDFTSVSSIMYILLVFLTMLIEMITC 180
 QY 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215
 Db 181 YRKVSKAEBAQENASDYLAIPSENKENSAPVEE 215
 RESULT 9
 ID AAM79212 standard; protein; 195 AA.
 XX
 XX AAM79212
 FH Domain 68.. 64
 FT

XX AAM79212;
AC
XX 06-NOV-2001 (first entry)
DT
XX Human protein SEQ ID NO 1874.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX
XX N-PSDB; AAK52345.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX
XX Claim 20; Page 4260; 6221pp; English.
XX
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM79323-AAK80102) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoietic regulatory
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibit activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Notes: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
SQ Sequence 195 AA;
Query Match 91.1%; Score 1024; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.7e-89;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 NVSRFEFEARHPVKTTRLPLRVTBAGDEFTSVSEIMYILLVFLTLLIEMIYC 180
OY 181 YRKVSKAEAAQENA 195
DB 181 YRKVSKAEAAQENA 195
RESULT 10
AAB50245
ID AAB50245 standard; protein, 191 AA.
XX
XX AAB50245;
XX
XX 13-MAR-2001 (first entry)
XX
XX
XX Rat sodium channel beta3 protein Alrx94h5 mature protein.
XX
XX Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction.
XX
XX Rattus sp.
XX
XX WO200069912-A1.
XX
XX 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013144.
XX
XX 14-MAY-1999; 99US-0134198P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI: 2001-122743/13.
XX
XX N-PSDB; AAC90600.
XX
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
XX root ganglion cDNA library for use in chromosome mapping, forensic
XX medicine, monitoring clinical trials and therapeutics.
XX
XX
XX Claim 9; Fig 2; 145pp; English.
XX
XX
XX The present invention provides the protein and coding sequences of the
XX rat sodium channel beta3 protein, designated Alrx94h5. This protein is
XX involved in the generation of pain and other sensory or perceptible nerve
XX impulses, in the establishment and endurance of mood, neurodegenerative
XX and sleep disorders, and in the control of muscle contraction, including
XX movements such as the heartbeat, digestion and vascular tone. The
XX sequences can be used in predictive medicine, screening and diagnostic
XX assays, and in pharmacogenomics
SQ Sequence 191 AA;
Query Match 87.7%; Score 986; DB 4; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.6e-85;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 11

ABG22577
ID ABG22577 standard; protein: 369 AA.

AC ABG22577;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22568.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

PI WPI; 2001-639362/73.

DR N-PADB; AAS86764.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 52936; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed Specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SO Sequence 369 AA;

Query Match 83.9%; Score 942.5; DB 4; Length 369;
Best Local Similarity 93.9%; Pred. No. 8.1e-81;
Matches 184; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 MPAFNRLPLASIVLIIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRBEVEATTV 59
DB 127 MPAFNRLPLASIVLIIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRBEVEATTV 186
QY 60 VEWFRPEGKDLIYERNQHVESPFQGRLOMNGSKDLQDVSIIVLNTINDSLYT 119

DB 187 VEWFRPEGKDLIYERNQHVESPFQGRLOMNGSKDLQDVSIIVLNTINDSLYT 246

QY 120 CWSRREFFFAHNPFKTTLPLPLRVTEAGDEPTSVSISIMYIILLVLTWLLIEMIX 179
DB 247 CWSRREFFFAHNPFKTTLPLPLRVTEAGDEPTSVSISIMYIILLVLTWLLIEMIX 306

QY 180 CYRKVSKEEPAQENA 195
DB 307 CYRKVSKEEPAQENA 322

RESULT 12

AAB36020
ID AAB36020 standard; protein: 159 AA.

AC AAB36020;

DT 15-FEB-2001 (first entry)

DE Human beta3 subunit peptide, SEQ ID NO: 22.

KW Human; beta sub-unit; beta3; analgesic; anticonvulsant;
KW cerebroprotective; vasotropic; cardiant; nootropic; cyostatic;
KW dermatological; gene therapy; voltage-gated sodium channel; pain;
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
KW familial nonchromaffin paraganglioma; phenylketonuria;
KW Charcot Marie Tooth disease.

OS Homo sapiens.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI WPI; 2000-665241/64.

DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
XX channel, and their corresponding polypeptides, useful for detecting and
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and
XX stroke.

PS Claim 36; Page 76; 88pp; English.

XX The present sequence is given in the claims of a specification relating
XX to a novel family of beta sub-unit proteins from a voltage-gated sodium
XX channel. Human and rat beta sub-units, which have been collectively
XX identified as beta3, have been isolated. The polynucleotides and
XX polypeptides are useful for screening for agonists and antagonists of
XX sodium channels. The agonists, antagonists, proteins and nucleic acids
XX may be used diagnosing of treating diseases or conditions associated with
XX voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
XX heart disease, Jacobsen Syndrome, familial Nonchromaffin Paraganglioma,
XX phenylketonuria and Charcot Marie Tooth disease

SO Sequence 159 AA;

Query Match 75.0%; Score 843; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 7.9e-72;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFNRLPLASIVLIIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRBEVEATTV 60
DB 1 MPAFNRLPLASIVLIIYWSVCPVCVEVSETEA-VQGNPMKLRCSCKRBEVEATTV 60

OY 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
DB 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
OY 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVSE 159
DB 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVSE 159

RESULT 13

ADSI0835
ID ADSI0835 standard; protein, 157 AA.

AC ADSI0835;

DT 16-DEC-2004 (first entry)

DE Human therapeutic protein - SEQ ID 1072.

KM antiinflammatory; neuroprotective; anti-naemic; cytoprotective; vulnary;
inflammation; haematopoiesis; immunity; neurodegenerative; stem cell;
aplastic anaemia; cancer; wound healing; gene therapy.

KM antiinflammatory; neuroprotective; anti-naemic; cytoprotective; vulnary;
inflammation; haematopoiesis; immunity; neurodegenerative; stem cell;
aplastic anaemia; cancer; wound healing; gene therapy.

OS Homo sapiens.

PN WO2004080148-A2.

PD 23-SEP-2004.

PF 30-SEP-2003; 2003WO-US030720.

PR 02-OCT-2002; 2002US-0416186P.

PA (NUVE-) NUVELO INC.

PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

DR MPI: 2004-668857/65.

DR N-PDB: ADSI0151.

PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

PS Claim 20; SEQ ID NO 1072; 718bp; English.

CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate anti-inflammatory,
CC neuroprotective, anti-naemic, cytoprotective and vulnary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX Sequence 157 AA;

XX Query Match 74.2%; Score 834; DB 8; Length 157;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-71;

XX Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPAENRLEPLASLVIYVSVCPVCEVPSBTEAVQGNPKMRLCISCMKREBEVATTVV 60
DB 1 MPAENRLEPLASLVIYVSVCPVCEVPSBTEAVQGNPKMRLCISCMKREBEVATTVV 60

OY 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
DB 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120

OY 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
DB 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120

OY 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVV 157
DB 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVV 157

RESULT 14

AAB36021
ID AAB36021 standard; protein, 159 AA.

AC AAB36021;

DT 15-FEB-2001 (first entry)

DE Rat beta3 subunit peptide, SEQ ID NO: 23.

KM Rat; beta subunit; beta3; analgesic; anticonvulsant; cerebroprotective;
vasotropic; cardiac; nootropic; cytoprotective; dermatological;
gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
ischemia; heart disease; Jacobsen Syndrome;
familial nonchromaffin paraganglioma; phenylketonuria;
Charcot Marie Tooth disease.

KM Rat; beta subunit; beta3; analgesic; anticonvulsant; cerebroprotective;
vasotropic; cardiac; nootropic; cytoprotective; dermatological;
gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
ischemia; heart disease; Jacobsen Syndrome;
familial nonchromaffin paraganglioma; phenylketonuria;
Charcot Marie Tooth disease.

KM Rat; beta subunit; beta3; analgesic; anticonvulsant; cerebroprotective;
vasotropic; cardiac; nootropic; cytoprotective; dermatological;
gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
ischemia; heart disease; Jacobsen Syndrome;
familial nonchromaffin paraganglioma; phenylketonuria;
Charcot Marie Tooth disease.

OS Rattus sp.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARIN) WARNER LAMBERT CO.
PA (WCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Cox P, Dixon A, Jackson A, Morgan K;

PI MPI: 2000-665241/64.

DR MPI: 2000-665241/64.

PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
PT stroke.

PS Claim 36; Page 76-77; 88bp; English.

CC The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease

XX Sequence 159 AA;

XX Query Match 74.0%; Score 832; DB 3; Length 159;

XX Best Local Similarity 98.7%; Pred. No. 8.8e-71;

XX Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MPAENRLEPLASLVIYVSVCPVCEVPSBTEAVQGNPKMRLCISCMKREBEVATTVV 60
DB 1 MPAENRLEPLASLVIYVSVCPVCEVPSBTEAVQGNPKMRLCISCMKREBEVATTVV 60

OY 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
DB 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120

OY 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120
DB 61 EMFYRPEGKDFLIYENYNGHOEVESPFQGRLONNGSKDLODVSTIVNTVLTNDGSLVTC 120

OY 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVSE 159
DB 121 NVSRFEFEFAHRPFVKYKTRLLIPLRVTEBAGDFTSVSE 159

DB 121 N/SREFEFAHRRPVKTRTLLPLRVTEAGEDEFTSVSE 159

RESULT 15

ABG22576
ID ABG22576 standard; protein; 1176 AA.

AC ABG22576;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22567.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR N-PSDB; AAS66763.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 52935; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX or sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AbG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1176 AA;

Query Match 61.7%; Score 694; DB 4; Length 1176;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VSYCFPVCEVPSSETAVQGNPKLRICISCMKREVEATTVEWFRPBGSKDPLIYEYR 78
DB 987 VSYCFPVCEVPSSETAVQGNPKLRICISCMKREVEATTVEWFRPBGSKDPLIYEYR 1046

QY 79 NGHVEVSPFQGRLOMNGSKDLQDVSIITVANTLNDGLYTCNVSRREFEFAHRRPVKTT 138
DB 1047 NGHVEVSPFQGRLOMNGSKDLQDVSIITVANTLNDGLYTCNVSRREFEFAHRRPVKTT 1106
QY 139 RLIPLRTEE 148
DB 1107 RLIPLRTEE 1116

Search completed: March 31, 2005, 20:17:51
Job time : 124.5 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:11:14 ; Search time 30 Seconds
(without alignments)
534.985 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLYWVS.....SDYLAIPEKENSAPVVEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | * Query Match | Length | DB ID | Description |
|------------|-------|------------------|--------|---------------------|-------------------|
| 1 | 470 | 41.8 | 204 | US-09-949-016-8240 | Sequence 8240, Ap |
| 2 | 147 | 13.1 | 215 | US-09-949-016-6658 | Sequence 6658, Ap |
| 3 | 147 | 13.1 | 263 | US-09-949-016-10819 | Sequence 10819, A |
| 4 | 131 | 11.7 | 269 | US-09-430-503-2 | Sequence 2, Appli |
| 5 | 131 | 11.7 | 269 | US-09-430-503-4 | Sequence 4, Appli |
| 6 | 131 | 11.7 | 269 | US-09-430-503-6 | Sequence 6, Appli |
| 7 | 131 | 11.7 | 269 | US-09-430-503-8 | Sequence 8, Appli |
| 8 | 131 | 11.7 | 313 | US-09-949-016-10974 | Sequence 10974, A |
| 9 | 129 | 11.5 | 199 | US-09-430-503-44 | Sequence 44, Appl |
| 10 | 129 | 11.5 | 199 | US-09-430-503-46 | Sequence 46, Appl |
| 11 | 127 | 11.3 | 199 | US-09-430-503-42 | Sequence 42, Appl |
| 12 | 127 | 11.3 | 199 | US-09-430-503-46 | Sequence 46, Appl |
| 13 | 127 | 11.3 | 209 | US-09-430-503-18 | Sequence 18, Appl |
| 14 | 127 | 11.3 | 209 | US-09-430-503-20 | Sequence 20, Appl |
| 15 | 127 | 11.3 | 209 | US-09-430-503-22 | Sequence 22, Appl |
| 16 | 127 | 11.3 | 209 | US-09-430-503-24 | Sequence 24, Appl |
| 17 | 125 | 11.1 | 270 | US-09-430-503-26 | Sequence 26, Appl |
| 18 | 125 | 11.1 | 270 | US-09-430-503-28 | Sequence 28, Appl |
| 19 | 125 | 11.1 | 270 | US-09-430-503-30 | Sequence 30, Appl |
| 20 | 125 | 11.1 | 270 | US-09-430-503-32 | Sequence 32, Appl |
| 21 | 118 | 10.5 | 159 | US-09-430-503-34 | Sequence 34, Appl |
| 22 | 118 | 10.5 | 159 | US-09-430-503-36 | Sequence 36, Appl |
| 23 | 118 | 10.5 | 159 | US-09-430-503-38 | Sequence 38, Appl |
| 24 | 118 | 10.5 | 159 | US-09-430-503-40 | Sequence 40, Appl |
| 25 | 112.5 | 9.8 | 215 | US-09-949-016-6523 | Sequence 6523, Ap |
| 26 | 110.5 | 9.8 | 225 | US-09-949-016-10820 | Sequence 10820, A |
| 27 | 110.5 | 9.8 | 225 | US-09-949-016-10820 | Sequence 10820, A |

| | | | | | |
|----|------|-----|-----|--------------------|-------------------|
| 28 | 109 | 9.7 | 344 | US-09-656-952-19 | Sequence 19, Appl |
| 29 | 109 | 9.7 | 394 | US-09-656-952-20 | Sequence 20, Appl |
| 30 | 109 | 9.7 | 394 | US-09-855-323-17 | Sequence 17, Appl |
| 31 | 108 | 9.6 | 801 | US-09-383-630-6 | Sequence 6, Appli |
| 32 | 106 | 9.4 | 519 | US-08-996-338-21 | Sequence 21, Appl |
| 33 | 106 | 9.4 | 519 | US-09-556-972-21 | Sequence 21, Appl |
| 34 | 106 | 9.4 | 537 | US-08-604-333-4 | Sequence 4, Appli |
| 35 | 106 | 9.4 | 537 | US-09-110-618-4 | Sequence 4, Appli |
| 36 | 106 | 9.4 | 537 | US-09-173-151A-29 | Sequence 29, Appl |
| 37 | 106 | 9.4 | 537 | US-09-578-178-4 | Sequence 4, Appli |
| 38 | 106 | 9.4 | 537 | US-09-577-806-4 | Sequence 4, Appli |
| 39 | 106 | 9.4 | 537 | US-09-621-502-8 | Sequence 8, Appli |
| 40 | 99.5 | 8.9 | 471 | US-09-949-016-9042 | Sequence 9042, Ap |
| 41 | 99.5 | 8.9 | 471 | US-09-949-016-9043 | Sequence 9043, Ap |
| 42 | 99.5 | 8.9 | 471 | US-09-949-016-9044 | Sequence 9044, Ap |
| 43 | 99.5 | 8.9 | 471 | US-09-949-016-9045 | Sequence 9045, Ap |
| 44 | 99.5 | 8.9 | 471 | US-09-949-016-9046 | Sequence 9046, Ap |
| 45 | 99.5 | 8.9 | 471 | US-09-949-016-9047 | Sequence 9047, Ap |

ALIGNMENTS

RESULT 1

US-09-949-016-8240

Sequence 8240, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8240

LENGTH: 204

TYPE: PRT

ORGANISM: Human

US-09-949-016-8240

Query Match 41.8%; Score 470; DB 4; Length 204;

Best Local Similarity 51.0%; Pred. No. 1.2e-42;

Matches 101; Conservative 30; Mismatches 59; Indels 8; Gaps 5;

QY 26 CVEVPSETEAVQGNPMKLRCSCKREVEATTVWVFYRPEGKQFL-IVERYNGHOEV 84

DB 7 CVEDSTETAVYQMTFPLICISCKRSEETAFFETFPQKGEERVKILRANEVLQ 66

QY 85 ESP-FOGRLQNGS---KQLODVSTLVNLTANDGLYTCNVSRPEFAHAPFVKTR 139

DB 67 EEDERFEGRVNNGSRGTQLODISIFITVTYNHSDYCHVYRLFFPENYEHTSVVK 126

QY 140 LIPLRVTEEGEDFTSVSEIMMYTLLVPLTLTLEMICYKRVSKA-DEAAQENASDY 198

DB 127 KIHLEVDKNNRMASIVSEIMMYTLLVPLTLVAVEMICYKRIATATTAQENASEY 186

QY 199 LAIPSENKEN-SAPVVEE 215

DB 187 LAITSEKENCCTGVVAE 204

RESULT 2

US-09-949-016-6658

Sequence 6658, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6658
LENGTH: 215
TYPE: PRT
ORGANISM: Human
US-09-949-016-6658

Query Match 13.1%; Score 147; DB 4; Length 215;
Best Local Similarity 25.7%; Pred. No. 9.6e-08;
Matches 57; Conservative 35; Mismatches 80; Indels 50; Gaps 9;

QY 7 LPLASLVLIYVWVCFPVCEVPSBTEAVQGNPMKLRICSCMKREBEVATTVMFYRP 66
DB 21 LMPILAA-VEIYTSRV-----LEAVNGTDARLKCTSSPAVGDALVT-MNFRP 67
QY 67 -EGG-KDPLIYERNQHGVESPFQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSR 124
DB 68 LDGGEQGFVYHHIDPFQPMGRFDRVSWDGNPBRYPASILLMKLQFDNDGTTCQVKN 127
QY 125 EPEFAHRPFVKTTRLILPRTVEAGEDEFTSVV-----SEIMMYILV-----FLTML 173
DB 128 -----PPDVGVIGEIRLSVHTVVRSEIHFLALAGSACALMIITVI 170
QY 174 LIEMTYCYRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
DB 171 VVLFQHYRKKRWABRA-----HKVVEIKSEEBRLNOK 205

RESULT 3
US-09-949-016-10819
Sequence 10819, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10819
LENGTH: 263
TYPE: PRT
ORGANISM: Human
US-09-949-016-10819

Query Match 13.1%; Score 147; DB 4; Length 263;
Best Local Similarity 25.7%; Pred. No. 1.3e-07;
Matches 57; Conservative 35; Mismatches 80; Indels 50; Gaps 9;

QY 7 LPLASLVLIYVWVCFPVCEVPSBTEAVQGNPMKLRICSCMKREBEVATTVMFYRP 66
DB 21 LMPILAA-VEIYTSRV-----LEAVNGTDARLKCTSSPAVGDALVT-MNFRP 67

DB 69 LMPILAA-VEIYTSRV-----LEAVNGTDARLKCTSSPAVGDALVT-MNFRP 115
QY 67 -EGG-KDPLIYERNQHGVESPFQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSR 124
DB 116 LDGGEQGFVYHHIDPFQPMGRFDRVSWDGNPBRYPASILLMKLQFDNDGTTCQVKN 175
QY 125 EPEFAHRPFVKTTRLILPRTVEAGEDEFTSVV-----SEIMMYILV-----FLTML 173
DB 176 -----PPDVGVIGEIRLSVHTVVRSEIHFLALAGSACALMIITVI 170
QY 174 LIEMTYCYRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
DB 219 VVLFQHYRKKRWABRA-----HKVVEIKSEEBRLNOK 253

RESULT 4
US-09-430-503-2
Sequence 2, Application US/09430503
Patent No. 6355786
GENERAL INFORMATION:
APPLICANT: Zhao, Zhizhuang
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
CURRENT APPLICATION NUMBER: US/09/430,503
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 269
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-503-2

Query Match 11.7%; Score 131; DB 3; Length 269;
Best Local Similarity 23.0%; Pred. No. 7.1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVSSETEAVQGNPMKLRICSCMKREBEVAT--TVVEMFYRPGSGKFL-IYERNQH 82
DB 40 VYTRKEIRIVANGTGKRLC-----KFKSITTGILTSVMSQPGSGADTVSFFHSGQOV 95
QY 83 EVES--PFQGRLOWNGSKLDQVSTIVLNTLNDGLTYCNVSRPEFAHRPFVKTTRL 140
DB 96 YLGVPFPFKRDISWAGDDKDKDASINIENMOFHHGTVCVKN----- 139
QY 141 IPLRTEAGEDEFTSVSE-----IMMYILVFLTMLIEMTYC--YRK----- 183
DB 140 -PPDIVQPGHRIRLVYVEKENLPVFPVWVVGIVAVLGLTLISMLAVLYRKNOKSR 198
QY 184 -----VSKAEAAQENASD-----YLAIPSENKENSAPVEE 211
DB 199 DYTGSTSESLSPVKQAPRKPSPDTEGLVKSLLPSGSHGCPVI 240

RESULT 5
US-09-430-503-4
Sequence 4, Application US/09430503
Patent No. 6355786
GENERAL INFORMATION:
APPLICANT: Zhao, Zhizhuang
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
CURRENT APPLICATION NUMBER: US/09/430,503
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 269
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-503-4

Query Match 11.7%; Score 131; DB 3; Length 269;
Best Local Similarity 23.0%; Pred. No. 7,1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPESETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82
DB 40 VYTPKEIFVANGQKLTCTC---KFKSTSTGGLTSVMSFQEGADTVTSFFHYSGQV 95
QY 83 EVES--PFOGRLQWNGSKLDQVSIIVLNTLNDGSLYTCNVSRFEFEAHRPFVKTRL 140
DB 96 YLGNYPFPKORISWAGDLKDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183
DB 140 -PPDIVQPGHIRLYVEKENLVPFVWVVGIVTAVLGLTLLISMLAVLYRRKNSKR 198
QY 184 -----VSKAEBAQENASD---YLAIPSENKENS AV 211
DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLPSGSHQGPVI 240

RESULT 6
US-09-430-503-6
Sequence 6, Application US/09430503
Patent No. 6355786
GENERAL INFORMATION:

APPLICANT: Zhao, Zhichuang
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
CURRENT APPLICATION NUMBER: US/09/430,503
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 269
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-503-6

Query Match 11.7%; Score 131; DB 3; Length 269;
Best Local Similarity 23.0%; Pred. No. 7,1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPESETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82
DB 40 VYTPKEIFVANGQKLTCTC---KFKSTSTGGLTSVMSFQEGADTVTSFFHYSGQV 95
QY 83 EVES--PFOGRLQWNGSKLDQVSIIVLNTLNDGSLYTCNVSRFEFEAHRPFVKTRL 140
DB 96 YLGNYPFPKORISWAGDLKDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183
DB 140 -PPDIVQPGHIRLYVEKENLVPFVWVVGIVTAVLGLTLLISMLAVLYRRKNSKR 198
QY 184 -----VSKAEBAQENASD---YLAIPSENKENS AV 211
DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLPSGSHQGPVI 240

RESULT 7
US-09-430-503-8
Sequence 8, Application US/09430503
Patent No. 6355786
GENERAL INFORMATION:
APPLICANT: Zhao, Zhichuang
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
CURRENT APPLICATION NUMBER: US/09/430,503
CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 269
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-503-8

Query Match 11.7%; Score 131; DB 3; Length 269;
Best Local Similarity 23.0%; Pred. No. 7,1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPESETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82
DB 40 VYTPKEIFVANGQKLTCTC---KFKSTSTGGLTSVMSFQEGADTVTSFFHYSGQV 95
QY 83 EVES--PFOGRLQWNGSKLDQVSIIVLNTLNDGSLYTCNVSRFEFEAHRPFVKTRL 140
DB 96 YLGNYPFPKORISWAGDLKDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183
DB 140 -PPDIVQPGHIRLYVEKENLVPFVWVVGIVTAVLGLTLLISMLAVLYRRKNSKR 198
QY 184 -----VSKAEBAQENASD---YLAIPSENKENS AV 211
DB 199 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLPSGSHQGPVI 240

RESULT 8
US-09-949-016-10974
Sequence 10974, Application US/09949016
Patent No. 6812335
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10974
LENGTH: 313
TYPE: PRT
ORGANISM: Human
US-09-949-016-10974

Query Match 11.7%; Score 131; DB 4; Length 313;
Best Local Similarity 23.0%; Pred. No. 8,8e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;

QY 27 VEVPESETEAVQGNPMKLCISCMKREVEAT--TVVEWYRPEGKDFL-IYEYRNGHQ 82
DB 84 VYTPKEIFVANGQKLTCTC---KFKSTSTGGLTSVMSFQEGADTVTSFFHYSGQV 139
QY 83 EVES--PFOGRLQWNGSKLDQVSIIVLNTLNDGSLYTCNVSRFEFEAHRPFVKTRL 140
DB 140 YLGNYPFPKORISWAGDLKDKDASININEMQFIHNGTYICDVKN-----183
QY 141 IPLRTEAGEDFTSVSE-----IMMYILVFLTLLIEMIYC--YRK-----183
DB 184 -PPDIVQPGHIRLYVEKENLVPFVWVVGIVTAVLGLTLLISMLAVLYRRKNSKR 242
QY 184 -----VSKAEBAQENASD---YLAIPSENKENS AV 211
DB 243 DYTGCSTSESLSPVKAQPRKSPDTEGLVKSLPSGSHQGPVI 284

RESULT 9
US-09-430-503-44
; Sequence 44, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-44

Query Match 11.5%; Score 129; DB 3; Length 199;
Best Local Similarity 26.0%; Pred. No. 7.5e-06;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREVEAT--TVEMFYRPEGKDFL-IYERYNGHQ 82
DB 40 VYTPKEIFVANGTGKLTG---KFKSTSTTGGLTSVMSFQPEGADTTVSFFHYSQGOV 95
QY 83 EVES--PQGRLOMNGSKDLOVSIIVLVNTLNDGSLYTCNVSRFEFEAHRPFVKTRRL 140
DB 96 YIGNVPPEKDRISWAGDLDKDKDASINIEHQFIHNGTYICVKN----- 139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLISMLAVLYRRKSKR 198
QY 188 E 188
DB 199 D 199

RESULT 10
US-09-430-503-48
; Sequence 48, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-48

Query Match 11.5%; Score 129; DB 3; Length 199;
Best Local Similarity 26.0%; Pred. No. 7.5e-06;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREVEAT--TVEMFYRPEGKDFL-IYERYNGHQ 82
DB 40 VYTPKEIFVANGTGKLTG---KFKSTSTTGGLTSVMSFQPEGADTTVSFFHYSQGOV 95
QY 83 EVES--PQGRLOMNGSKDLOVSIIVLVNTLNDGSLYTCNVSRFEFEAHRPFVKTRRL 140
DB 96 YIGNVPPEKDRISWAGDLDKDKDASINIEHQFIHNGTYICVKN----- 139

QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLISMLAVLYRRKSKR 198
QY 188 E 188
DB 199 D 199

RESULT 11
US-09-430-503-42
; Sequence 42, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-42

Query Match 11.3%; Score 127; DB 3; Length 199;
Best Local Similarity 26.0%; Pred. No. 1.2e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREVEAT--TVEMFYRPEGKDFL-IYERYNGHQ 82
DB 40 VYTPKEIFVANGTGKLTG---KFKSTSTTGGLTSVMSFQPEGADTTVSFFHYSQGOV 95
QY 83 EVES--PQGRLOMNGSKDLOVSIIVLVNTLNDGSLYTCNVSRFEFEAHRPFVKTRRL 140
DB 96 YIGNVPPEKDRISWAGDLDKDKDASINIEHQFIHNGTYICVKN----- 139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTMLLIMTYCY---RKVSKA 187
DB 140 -PPDIVQPGHIRLYVEKENLPVFPVWVVGIVTAVVLGLTLISMLAVLYRRKSKR 198
QY 188 E 188
DB 199 D 199

RESULT 12
US-09-430-503-46
; Sequence 46, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-46

Query Match 11.3%; Score 127; DB 3; Length 199;
Best Local Similarity 26.0%; Pred. No. 1.2e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSETEAVQGNPMKLRICISCMKREVEAT--TVEMFYRPEGKDFL-IYERYNGHQ 82

Db 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTGGTTSVSMSPQEGADTTVSFFHYSGQV 95
QY 83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSRFEFEFAHRRPVKTRLL 140
Db 96 YLGNYPFPKDRISMAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTLMLEIMICY--RKVSKA 187
Db 140 -PPDIVVQPGHTRLYVEKENLVPFPVWVVGIVTAVVLGLTLLISMILAVLYRRKNSKR 198
QY 188 E 188
Db 199 D 199

RESULT 13
US-09-430-503-18
; Sequence 18, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-18

Query Match 11.3%; Score 127; DB 3; Length 209;
Best Local Similarity 26.0%; Pred. No. 1.3e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSSETAVQGNPMKLRICISCKRREVEAT--TVWEFYPREGGKDFL-IYEYRNHQ 82
Db 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTGGTTSVSMSPQEGADTTVSFFHYSGQV 95
QY 83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSRFEFEFAHRRPVKTRLL 140
Db 96 YLGNYPFPKDRISMAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTLMLEIMICY--RKVSKA 187
Db 140 -PPDIVVQPGHTRLYVEKENLVPFPVWVVGIVTAVVLGLTLLISMILAVLYRRKNSKR 198
QY 188 E 188
Db 199 D 199

RESULT 14
US-09-430-503-20
; Sequence 20, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-430-503-20

Query Match 11.3%; Score 127; DB 3; Length 209;
Best Local Similarity 26.0%; Pred. No. 1.3e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSSETAVQGNPMKLRICISCKRREVEAT--TVWEFYPREGGKDFL-IYEYRNHQ 82
Db 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTGGTTSVSMSPQEGADTTVSFFHYSGQV 95
QY 83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSRFEFEFAHRRPVKTRLL 140
Db 96 YLGNYPFPKDRISMAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTLMLEIMICY--RKVSKA 187
Db 140 -PPDIVVQPGHTRLYVEKENLVPFPVWVVGIVTAVVLGLTLLISMILAVLYRRKNSKR 198
QY 188 E 188
Db 199 D 199

RESULT 15
US-09-430-503-22
; Sequence 22, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-22

Query Match 11.3%; Score 127; DB 3; Length 209;
Best Local Similarity 26.0%; Pred. No. 1.3e-05;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;

QY 27 VEVPSSETAVQGNPMKLRICISCKRREVEAT--TVWEFYPREGGKDFL-IYEYRNHQ 82
Db 40 VYTPKEIFVANGTQGLTCTC---KFKSTSTGGTTSVSMSPQEGADTTVSFFHYSGQV 95
QY 83 EVES--PFGRLQWNGSKLDQVSTIVLVNTLNDGSLYTCNVSRFEFEFAHRRPVKTRLL 140
Db 96 YLGNYPFPKDRISMAGDLDKDASININEMQFIHNGTYICDVKN-----139
QY 141 IPLRVTEAGDEFTSVSE-----IMMYILLVFLTLMLEIMICY--RKVSKA 187
Db 140 -PPDIVVQPGHTRLYVEKENLVPFPVWVVGIVTAVVLGLTLLISMILAVLYRRKNSKR 198
QY 188 E 188
Db 199 D 199

Search completed: March 31, 2005, 20:23:54
Job time: 30 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:21:59 ; Search time 91.5 Seconds
(without alignments)
779.153 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124

Sequence: 1 MPAENRLLPLASIVLTYWVS.....SDYLAIPEKENSAPVEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Published Applications AA:*

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PC7_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppa/PC7US_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
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13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
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19: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1124 | 100.0 | 215 | 11 | US-09-977-579-2 |
| 2 | 1124 | 100.0 | 215 | 14 | US-10-142-201B-11 |
| 3 | 1105 | 98.3 | 215 | 11 | US-09-977-579-1 |
| 4 | 1105 | 98.3 | 215 | 13 | US-10-029-191-2 |
| 5 | 1105 | 98.3 | 215 | 13 | US-10-142-201B-12 |
| 6 | 986 | 87.7 | 191 | 13 | US-10-029-191-4 |
| 7 | 983 | 75.0 | 159 | 11 | US-09-977-579-22 |
| 8 | 832 | 74.0 | 159 | 11 | US-09-977-579-23 |
| 9 | 597 | 53.1 | 111 | 13 | US-10-029-191-5 |
| 10 | 477 | 42.4 | 218 | 13 | US-10-029-191-20 |
| 11 | 472 | 42.0 | 218 | 11 | US-09-977-579-44 |
| 12 | 471 | 41.9 | 218 | 14 | US-10-142-201B-8 |
| 13 | 471 | 41.9 | 218 | 16 | US-10-477-272-2 |

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|----|-------|------|-----|----|--------------------|-------------------|
| 14 | 282 | 25.1 | 58 | 13 | US-10-029-191-7 | Sequence 7, Appl |
| 15 | 258.5 | 23.0 | 268 | 9 | US-09-875-456A-14 | Sequence 14, Appl |
| 16 | 258.5 | 23.0 | 268 | 15 | US-10-401-916-14 | Sequence 14, Appl |
| 17 | 234 | 20.8 | 74 | 15 | US-10-276-774-2068 | Sequence 2068, Ap |
| 18 | 207 | 18.4 | 39 | 11 | US-09-977-579-17 | Sequence 17, Appl |
| 19 | 196 | 17.4 | 39 | 11 | US-09-977-579-18 | Sequence 18, Appl |
| 20 | 167 | 14.9 | 248 | 15 | US-10-205-331-110 | Sequence 110, App |
| 21 | 165 | 14.7 | 34 | 11 | US-09-977-579-31 | Sequence 31, Appl |
| 22 | 163.5 | 14.5 | 248 | 15 | US-10-016-248-54 | Sequence 54, Appl |
| 23 | 163.5 | 14.5 | 251 | 15 | US-10-016-248-52 | Sequence 52, Appl |
| 24 | 163.5 | 14.5 | 258 | 15 | US-10-016-248-53 | Sequence 53, Appl |
| 25 | 161 | 14.3 | 34 | 11 | US-09-977-579-47 | Sequence 47, Appl |
| 26 | 160.5 | 14.3 | 235 | 13 | US-10-053-107-12 | Sequence 12, Appl |
| 27 | 160.5 | 14.3 | 235 | 14 | US-10-227-884-238 | Sequence 238, App |
| 28 | 160.5 | 14.3 | 235 | 14 | US-10-230-163-238 | Sequence 238, App |
| 29 | 160.5 | 14.3 | 235 | 14 | US-10-230-338-238 | Sequence 238, App |
| 30 | 160.5 | 14.3 | 235 | 14 | US-10-218-631-238 | Sequence 238, App |
| 31 | 160.5 | 14.3 | 235 | 14 | US-10-230-414-238 | Sequence 238, App |
| 32 | 160.5 | 14.3 | 235 | 14 | US-10-213-145-12 | Sequence 12, Appl |
| 33 | 160.5 | 14.3 | 235 | 14 | US-10-232-224-238 | Sequence 238, App |
| 34 | 160.5 | 14.3 | 235 | 14 | US-10-216-158A-238 | Sequence 238, App |
| 35 | 160.5 | 14.3 | 235 | 14 | US-10-218-849-238 | Sequence 238, App |
| 36 | 160.5 | 14.3 | 235 | 14 | US-10-227-873-238 | Sequence 238, App |
| 37 | 160.5 | 14.3 | 235 | 14 | US-10-227-883-238 | Sequence 238, App |
| 38 | 160.5 | 14.3 | 235 | 14 | US-10-219-076-238 | Sequence 238, App |
| 39 | 160.5 | 14.3 | 235 | 14 | US-10-230-434-238 | Sequence 238, App |
| 40 | 160.5 | 14.3 | 235 | 14 | US-10-213-199-12 | Sequence 12, Appl |
| 41 | 160.5 | 14.3 | 235 | 14 | US-10-219-003-238 | Sequence 238, App |
| 42 | 160.5 | 14.3 | 235 | 14 | US-10-219-075-238 | Sequence 238, App |
| 43 | 160.5 | 14.3 | 235 | 14 | US-10-219-464-238 | Sequence 238, App |
| 44 | 160.5 | 14.3 | 235 | 14 | US-10-219-466-238 | Sequence 238, App |
| 45 | 160.5 | 14.3 | 235 | 14 | US-10-219-479-238 | Sequence 238, App |

ALIGNMENTS

RESULT 1
US-09-977-579-2
Sequence 2, Application US/09977579
Publication No. US20040248240A1
GENERAL INFORMATION:
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
TITLE OF INVENTION: Channel
FILE REFERENCE: 674558-2001
CURRENT APPLICATION NUMBER: US/09/977, 579
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/EP00/01783
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60,129,473
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-579-2

Query Match 100.0%; Score 1124; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.9e-104;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAENRLLPLASIVLTYWVS...PVCVPEVSETEAVQGNPMKURCTSCMKREBEATTVV 60
DB 1 MPAENRLLPLASIVLTYWVS...PVCVPEVSETEAVQGNPMKURCTSCMKREBEATTVV 60
QY 61 EWFYREGGKDFILTYEYRNGHGVESPPQGRLLQWNSKDLQDVSTVLVNTLNDGLYTC 120
DB 61 EWFYREGGKDFILTYEYRNGHGVESPPQGRLLQWNSKDLQDVSTVLVNTLNDGLYTC 120

| QY | 122 | NSRSEEPFAHPPYKXTRILPLRATSEAGDEPFSVSEIMMYTLVFLTMLIENIYC | 180 |
|----|---|---|-----|
| Db | 121 <td>NSRSEEPFAHPPYKXTRILPLRATSEAGDEPFSVSEIMMYTLVFLTMLIENIYC <th>180</th> </td> | NSRSEEPFAHPPYKXTRILPLRATSEAGDEPFSVSEIMMYTLVFLTMLIENIYC <th>180</th> | 180 |
| QY | 181 | YRKYSTAEBAAQBNASDYLAIPSENKENSAYPVEE | 215 |
| Db | 181 | YRKYSTAEBAAQBNASDYLAIPSENKENSAYPVEE | 215 |

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RESULT 2
US-10-142-201B-11
; Sequence 11, Application US/10142201B
; Publication No. US20030022205A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 98359, A SODIUM CHANNEL
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP12001-106P1RN(M)
; CURRENT APPLICATION NUMBER: US/10/142, 201B
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/289,893
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-142-201B-11

```

ORGANISM: Rat
US-09-977-579-1

| Query Match | Similarity | 98.3% | Score 1105 | DB 11 | Length 215 |
|-------------|------------|---|--------------------|------------|------------|
| Best Local | Similarity | 98.1% | Pred. No. 1.5e-102 | | |
| Matches | 211 | Conservative | 0 | Mismatches | 4 |
| | | | | Indels | 0 |
| | | | | Gaps | 0 |
| QY | 1 | MPAFNRLEPLASLVIILVWVSCFPCVCEVSEBTEAVQGNPMKLRICISCKRKEEVEATTVV | 60 | | |
| Db | 1 | MPAFNRRLPLPLASLVIILVWVRCVFCVCEVSEBTEAVQGNPMKLRICISCKRKEEVEATTVV | 60 | | |
| QY | 61 | EMFPRPEGCKGFLIYERYNGHOEVESPQGRLOWNGSKDLODVSTLVNTLVNTDLSGLYTC | 120 | | |
| Db | 61 | EMFPRPEGCKGFLIYERYNGHOEVESPQGRLOWNGSKDLODVSTLVNTLVNTDLSGLYTC | 120 | | |
| QY | 121 | NVSEEFEEFAHRPVKTRLLPLRVTEBAGEDFTSVSEIMMYILLVPLTLLILBMYTC | 180 | | |
| Db | 121 | NVSEEFEEFAHRPEVKTRLLPLRVTEBAGEDFTSVSEIMMYILLVPLTLLILBMYTC | 180 | | |
| QY | 181 | YRKVSKAEAAQENASDYLAIPESEKESAVPVVE | 215 | | |
| Db | 181 | YRKVSKAEAAQENASDYLAIPESEKESAVPVVE | 215 | | |

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RESULT 4
US-10-029-191-2
; Sequence 2, Application US/10029191
; Publication No. US2002016045A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL, BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-2

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; NUMBER OF SEQ. ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRN
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APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A. J.
TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT.
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MPI2001-106P(RN/IM)
CURRENT APPLICATION NUMBER: US/10/142, 201B
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289, 893
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 215
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-142-201B-12

Query Match 98.3%; Score 1105; DB 14; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.5e-102;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLITWVSCFPCVCPVSETEAVOGNPMKLCISCMKREVEATTVV 60
DB 1 MPANRLPLASLVLITWVSCFPCVCPVSETEAVOGNPMKLCISCMKREVEATTVV 60
QY 61 EMFRRPGGKDFLIYERNGHOEVSPFOGRLQWNGSKDLDVSIITVLTNDSGLYTC 120
DB 61 EMFRRPGGKDFLIYERNGHOEVSPFOGRLQWNGSKDLDVSIITVLTNDSGLYTC 120
QY 121 NVSREFEFAHRRPVTTRILIPRVTEAGEDEFTSVSEIMMYTLVFLTMLIEMIYC 180
DB 121 NVSREFEFAHRRPVTTRILIPRVTEAGEDEFTSVSEIMMYTLVFLTMLIEMIYC 180
QY 181 YRKVSKAEBAOENASDYLAIPSENKENSAPVVEE 215
DB 181 YRKVSKAEBAOENASDYLAIPSENKENSAPVVEE 215

RESULT 6
US-10-029-191-4
Sequence 4, Application US/10029191
Publication No. US20020160453A1
GENERAL INFORMATION:
APPLICANT: CURTIS, RORY A. J.
TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 210147.00XX/501
CURRENT APPLICATION NUMBER: US/10/029, 191
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 09/569, 978
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/134, 198
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 191
TYPE: PRT
ORGANISM: Rattus sp.
US-10-029-191-4

Query Match 87.7%; Score 986; DB 13; Length 191;
Best Local Similarity 99.0%; Pred. No. 1.2e-90;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 VCVEVSETEAVOGNPMKLCISCMKREVEATTVVEMFRRPGGKDFLIYERNGHOEV 84
DB 1 VCVEVSETEAVOGNPMKLCISCMKREVEATTVVEMFRRPGGKDFLIYERNGHOEV 60
QY 85 ESPFOGRLQWNGSKDLDVSIITVLTNDSGLYTCVNSREFEFAHRRPVTTRILIPR 144
DB 61 ESPFOGRLQWNGSKDLDVSIITVLTNDSGLYTCVNSREFEFAHRRPVTTRILIPR 120

QY 145 VTEAGEDEFTSVSEIMMYTLVFLTMLIEMIYCYRKVSKAEBAOENASDYLAIPSE 204
DB 121 VTEAGEDEFTSVSEIMMYTLVFLTMLIEMIYCYRKVSKAEBAOENASDYLAIPSE 180
QY 205 NKENSAPVVEE 215
DB 181 NKENSAPVVEE 191

RESULT 7
US-09-977-579-22
Sequence 22, Application US/09977579
Publication No. US20040248240A1
GENERAL INFORMATION:
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
TITLE OF INVENTION: channel
FILE REFERENCE: 674558-2001
CURRENT APPLICATION NUMBER: US/09/977, 579
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/EP00/01783
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60,129,473
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-579-22

Query Match 75.0%; Score 843; DB 11; Length 159;
Best Local Similarity 100.0%; Pred. No. 2e-76;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLITWVSCFPCVCPVSETEAVOGNPMKLCISCMKREVEATTVV 60
DB 1 MPANRLPLASLVLITWVSCFPCVCPVSETEAVOGNPMKLCISCMKREVEATTVV 60
QY 61 EMFRRPGGKDFLIYERNGHOEVSPFOGRLQWNGSKDLDVSIITVLTNDSGLYTC 120
DB 61 EMFRRPGGKDFLIYERNGHOEVSPFOGRLQWNGSKDLDVSIITVLTNDSGLYTC 120
QY 121 NVSREFEFAHRRPVTTRILIPRVTEAGEDEFTSVSE 159
DB 121 NVSREFEFAHRRPVTTRILIPRVTEAGEDEFTSVSE 159

RESULT 8
US-09-977-579-23
Sequence 23, Application US/09977579
Publication No. US20040248240A1
GENERAL INFORMATION:
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
TITLE OF INVENTION: channel
FILE REFERENCE: 674558-2001
CURRENT APPLICATION NUMBER: US/09/977, 579
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/EP00/01783
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60,129,473
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 159
TYPE: PRT
ORGANISM: Rat
US-09-977-579-23

Query Match 74.0%; Score 832; DB 11; Length 159;
Best Local Similarity 98.7%; Pred. No. 2.6e-75;
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFAFNRLPLALVLIYWSVCPVCEVPEVSETEAVOQNPMLKRCISCKMKEVEATTVV 60
DB 1 MFAFNRLPLALVLIYWSVCPVCEVPEVSETEAVOQNPMLKRCISCKMKEVEATTVV 60
QY 61 EWFYRPEGKDFLIYERNGHOVESPFQGRLOMNGSKDLODVSTVLNVTLNDGSLYTC 120
DB 61 EWFYRPEGKDFLIYERNGHOVESPFQGRLOMNGSKDLODVSTVLNVTLNDGSLYTC 120
QY 121 NVSRFEFEARHPFVKTRTLPRLRYTEAGDEFTSVSE 159
DB 121 NVSRFEFEARHPFVKTRTLPRLRYTEAGDEFTSVSE 159

RESULT 9

US-10-029-191-5
; Sequence 5, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-5

Query Match 53.1%; Score 597; DB 13; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.3e-52;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 VCVEVPESETEAVOQNPMLKRCISCKMKEVEATTVVEMFYRPEGKDFLIYERNGHOEV 84
DB 1 VCVEVPESETEAVOQNPMLKRCISCKMKEVEATTVVEMFYRPEGKDFLIYERNGHOEV 60
QY 85 ESWFQGRLOMNGSKDLODVSTVLNVTLNDGSLYTCNVSREPEFAHRPFV 135
DB 61 ESWFQGRLOMNGSKDLODVSTVLNVTLNDGSLYTCNVSREPEFAHRPFV 111

RESULT 10

US-10-029-191-20
; Sequence 20, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 218

TYPE: PRT
; ORGANISM: Lepus sp.
US-10-029-191-20

Query Match 42.4%; Score 477; DB 13; Length 218;
Best Local Similarity 49.5%; Pred. No. 1.7e-39;
Matches 106; Conservative 32; Mismatches 66; Indels 8; Gaps 5;

QY 10 LASLVLIYWSVCPVCEVPEVSETEAVOQNPMLKRCISCKMKEVEATTVVEMFYRPEG 69
DB 5 LAFVGAALVSSAWGCVPEVSETEAVYGMFKILICISCKRSETTAFTFEMTRQKGT 64
QY 70 KDFL-IYERNGHOVESPF--FQGRLOMNGS---KDLQDVSTVLNVTLNDGSLYTCNV 123
DB 65 EEFVKILRYENEVLQLEDERPEGRVWNGSRGTDLODLSIFITNVTYHNSGDYQCHVY 124
QY 124 REFEEARHPFVKTRTLPRLRYTEAGDEFTSVSEIMMYLILVPLTLMLEMTYCYRK 183
DB 125 RLSPFENYEHNTSVVKKIHLEVDYDANRDMASIVSEIMMYLILVPLTLMLEMTYCYRK 184
QY 184 VSKA-EBAAGENASDYLAIPSENKEN-SAPVVEE 215
DB 185 IAAATEAAAGENASEYLAITSESKENCTGVAAE 218

RESULT 11

US-09-977-579-44
; Sequence 44, Application US/09977579
; Publication No. US20040240240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Rat
US-09-977-579-44

Query Match 42.0%; Score 472; DB 11; Length 218;
Best Local Similarity 49.1%; Pred. No. 5.4e-39;
Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;

QY 10 LASLVLIYWSVCPVCEVPEVSETEAVOQNPMLKRCISCKMKEVEATTVVEMFYRPEG 69
DB 5 LALVGAALVSSAWGCVPEVSETEAVYGMFKILICISCKRSETTAFTFEMTRQKGT 64
QY 70 KDFL-IYERNGHOVESPF--FQGRLOMNGS---KDLQDVSTVLNVTLNDGSLYTCNV 123
DB 65 EEFVKILRYENEVLQLEDERPEGRVWNGSRGTDLODLSIFITNVTYHNSGDYQCHVY 124
QY 124 REFEEARHPFVKTRTLPRLRYTEAGDEFTSVSEIMMYLILVPLTLMLEMTYCYRK 183
DB 125 RLSPFENYEHNTSVVKKIHLEVDYDANRDMASIVSEIMMYLILVPLTLMLEMTYCYRK 184
QY 184 VSKA-EBAAGENASDYLAIPSENKEN-SAPVVEE 215
DB 185 IAAATEAAAGENASEYLAITSESKENCTGVAAE 218

RESULT 12

US-10-142-201B-8
; Sequence 8, Application US/10142201B

Search completed: March 31, 2005, 20:39:33
Job time : 92.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 20:10:33 ; Search time 26.5 Seconds

(without alignments)
780.627 Million cell updates/sec

Title: US-09-977-579-2

Sequence: 1 MPANFLPLSLVLIYWS.....SDYLAIPESENKSAVPVEE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 477 | 42.4 | 218 | 2 JC4788 | sodium channel pro |
| 2 | 472 | 42.0 | 218 | 2 A42737 | sodium channel, bet |
| 3 | 471 | 41.9 | 218 | 2 A55734 | sodium channel, vo |
| 4 | 175 | 15.6 | 248 | 1 MPRT0 | myelin P0 protein |
| 5 | 163.5 | 14.5 | 248 | 1 JH0252 | myelin P0 protein |
| 6 | 163.5 | 14.5 | 251 | 2 I38053 | myelin protein zer |
| 7 | 159 | 14.1 | 219 | 1 A29128 | myelin P0 protein |
| 8 | 154.5 | 13.7 | 247 | 1 A54662 | myelin P0 protein |
| 9 | 144.5 | 12.9 | 246 | 1 A32999 | myelin P0 protein |
| 10 | 140.5 | 12.5 | 249 | 1 A61087 | myelin P0 glycopro |
| 11 | 118 | 10.5 | 215 | 2 A57843 | sodium channel bet |
| 12 | 117 | 10.4 | 166 | 2 I61783 | sodium channel bet |
| 13 | 111.5 | 9.9 | 820 | 2 S17255 | fibroblast growth |
| 14 | 111.5 | 9.9 | 820 | 2 S17255 | fibroblast growth |
| 15 | 110.5 | 9.8 | 821 | 1 TVMSBK | protein-tyrosine-P |
| 16 | 109 | 9.7 | 1462 | 1 B36182 | fibroblast growth |
| 17 | 107 | 9.5 | 800 | 2 TVHUF | fibroblast growth |
| 18 | 107 | 9.5 | 801 | 2 I55363 | heparin-binding gr |
| 19 | 103.5 | 9.2 | 129 | 2 S57864 | T cell receptor W1 |
| 20 | 103.5 | 9.2 | 353 | 2 S51242 | heparin-binding fi |
| 21 | 103.5 | 9.2 | 372 | 2 C39371 | Ig V-region-like B |
| 22 | 101.5 | 9.0 | 806 | 2 A35963 | protein-tyrosine k |
| 23 | 100.5 | 8.9 | 750 | 2 S41051 | fibroblast growth |
| 24 | 99.5 | 8.9 | 131 | 2 B32513 | Ig kappa chain pre |
| 25 | 99.5 | 8.9 | 131 | 2 PT0178 | Ig kappa chain pre |
| 26 | 99.5 | 8.9 | 131 | 2 B30577 | Ig kappa chain pre |
| 27 | 98.5 | 8.8 | 118 | 2 TVHUF2 | fibroblast growth |
| 28 | 98.5 | 8.8 | 131 | 2 S24539 | Ig kappa chain V r |
| 29 | 98.5 | 8.8 | 131 | 2 D34904 | Ig kappa chain pre |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 98.5 | 8.8 | 748 | 2 S41050 | fibroblast growth |
| 31 | 98.5 | 8.8 | 823 | 2 B35963 | protein-tyrosine k |
| 32 | 98.5 | 8.8 | 1379 | 2 JC4954 | vascular endotheli |
| 33 | 97.5 | 8.7 | 118 | 2 S24533 | Ig kappa chain V r |
| 34 | 96 | 8.5 | 130 | 2 C29380 | Ig kappa chain pre |
| 35 | 96 | 8.5 | 136 | 2 S36320 | T-cell receptor de |
| 36 | 95.5 | 8.5 | 131 | 2 B39276 | Ig light chain pre |
| 37 | 95.5 | 8.5 | 707 | 2 A38429 | keratinocyte growt |
| 38 | 95.5 | 8.5 | 707 | 2 A54846 | fibroblast growth |
| 39 | 95.5 | 8.5 | 822 | 2 B54846 | fibroblast growth |
| 40 | 95.5 | 8.5 | 824 | 2 S24108 | protein-tyrosine k |
| 41 | 94.5 | 8.4 | 118 | 2 S24535 | Ig kappa chain V r |
| 42 | 94.5 | 8.4 | 118 | 2 S24500 | Ig kappa chain V r |
| 43 | 94.5 | 8.4 | 118 | 2 S24529 | Ig kappa chain V r |
| 44 | 94.5 | 8.4 | 131 | 2 B34904 | Ig kappa chain pre |
| 45 | 94.5 | 8.4 | 131 | 2 S09259 | Ig kappa chain pre |

ALIGNMENTS

RESULT 1

JC4788 sodium channel protein beta chain - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: JC4788

R:Belcher, S.M.; Howe, J.R.

Gene 170, 285-286, 1996

A:Title: Cloning of the cDNA encoding the sodium channel beta subunit from rabbit.

A:Reference number: JC4788; MUID:56235151; PMID:8666261

A:Accession: JC4788

A:Molecule type: mRNA

A:Residues: 1-218 <BEL>

A:Cross-references: UNIPROT:P53788; GB:U35382; NID:G1016013; PIDN:AAB17572.1; PID:G101601

A:Comment: This protein is composed of a large alpha-chain and two small beta-chains and

duction.

C:Genetics:

A:Gene: obet1

C:Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

F:161-182/Domain: transmembrane #status predicted <TM>

F:93,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.4%; Score 477; DB 2; Length 218;

Best Local Similarity 49.5%; Pred. No. 1,1e-33;

Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;

| | | | |
|----|-----|---|-----|
| Qy | 10 | IASIVLIYWSVCPVCEVPSSETEAVQGNPKLRICSCMKREBEATVVFPEEGG | 69 |
| Db | 5 | LAPVGGALVSSAMGCGVEVDSETEAVYGMTFKILICSCGRSEETETETETFRQKT | 64 |
| Qy | 70 | KDFL-IYEVNNGHVEESP--FQGRLOWNS---KDLQDVSTLVNLTNDGSLGTCNV | 123 |
| Db | 65 | EEFVFKILRYENEVLQLEEDERFEGRVVNGSRGKDLQDLSIFLTNTVYHNSGQYCHV | 124 |
| Qy | 124 | REEEFNAHPFVKTRILPIRVTBEAGEDFTSVSEETMTLLVFLTLLIEMTYCYRK | 183 |
| Db | 125 | RLTSFEYEINTSVKKIHLEVDVKANRDVASIVSEIMVYLIVLIVLVAEIVCYKK | 184 |
| Qy | 184 | VSRA-EEAQAENASDYLAIPSENKEN-SAVPVEE | 215 |
| Db | 185 | IAAATEAAQAENASDYLAIPSENKENCTGVQVAE | 218 |

RESULT 2

A42737 sodium channel beta 1 subunit - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A42737

R:Jiom, L.L.; De Jongh, K.S.; Patton, D.B.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa]

Science 256, 839-842, 1992

A:Title: Primary structure and functional expression of the beta 1 subunit of the rat br

A:Reference number: A42737; MUID:92271207; PMID:1375395
A:Accession: A42737
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-218 <ISO>
A:Cross-References: UNIPROT:Q00954; GB:M91808; NID:9206864; PIDN:AAA8513.1; PID:9206866
A:Experimental Source: Brain
A:Note: Sequence extracted from NCBI backbone (NCBIP:103298)
;Keywords: transmembrane protein

| | | | | |
|-----------------------|------------------|------------------|-----------|-------------|
| Query Match | 42.0%; | Score 472; | DB 2; | Length 218; |
| Best Local Similarity | 49.1%; | Pred. No. 3e-33; | | |
| Matches 105; | Conservative 33; | Mismatches 68; | Indels 8; | Gaps 57 |

| | | | |
|----|-----|---|-----|
| Oy | 10 | LASIVILIYVWSVCEPVCVPSETEVAOONPMKRLCISOMKREVEATTVEMFREGG | 69 |
| Db | 5 | LALVAGVALVSSAMGGCCVEVDSETEVAVMGTMLTLCISCRRSETTJMTFTMFROKGT | 64 |
| Oy | 70 | KDFL-YEYENRGHOEVESP--FGGRLOWNGS---KDLDVSITVLNLTANDSLGYTCNVS | 123 |
| Db | 65 | EELFKILIRYNEVLQLEEDDERPEGRVWVGSGSTGLDLDLSITINVTYNHSGPYECHVY | 124 |
| Oy | 124 | REEFEAPHREFVKTTLLIPLRYTEAGEDFTSVSEIMMYILLVFLLMLLIEMIYYCYRK | 183 |
| Db | 125 | RLLFPDYVENHTSVVKKIHLEVVDKXANRDMASIVSEIMMYVILVLTITWLVAEMVYCYKK | 184 |
| Oy | 184 | VSKA-EBAQENASDVLIATPSENKEN-SAVPPEE | 215 |
| Db | 185 | IAATEEAQAQENASEVYLATSISEKENCCTGVQAE | 218 |

RESULT 3
A55734.

sodium channel, voltage-gated, beta-1 chain precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
 C/Accession: A55734; A53108; I54354
 R/Makita, N.; Sloan-Brown, K.; Meghni, D.O.; Rogers, H.H.; George Jr., A.L.
 A/Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)
 C/Reference number: A55734; MUID:95154833; PMID:7851891
 A/Accession: A55734

A:Molecule type: DNA
A:Residues: 1-218 <MAK1>
A:Cross-references: UNIPROT:Q07699; GB:U12189
R:Mitla, N.; Bennett Jr., P.B.; George Jr., A.L.
J. Biol. Chem. 269, 7571-7578, 1994
A:Title: Voltage-gated Na(+) channel beta-1 subunit mRNA expressed in adult human skeletal muscle
A:Reference number: A53408; MUID:94171787; PMID:8125980
A:Accession: A53408
A:Molecule type: mRNA

A/Residues: 1-218 <MAK2>
A/Cross-references: GB:146242; NID:g450602; PIDN:AAA61277.1; PID:g450603
R/McLarchey, A.I.; Cannon, S.C.; Slaugenhaupt, S.A.; Gusella, J.F.
Hum. Mol. Genet. 2, 745-749, 1993
A/Title: The cloning and expression of a sodium channel beta 1-subunit cDNA from human brain
A/Reference number: 154354; MUID:93357746; PMID:8394762

A:Accession: 154354
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-218 <RES>
A:Cross-references: GB:J10338, NID:g307414, PIDN:AAA60391.1, PID:g307415

```

C/Gene: GDB:SCN1B
A/Cross-references: GDB:127281; OMIM:600235
A/Map position: 19q13.1-19q13.1
F/1.19/Domain: glycoprotein; muscle; transmembrane protein
C/Keywds: glycoprotein; muscle; transmembrane protein
F/1.1-182/Domain: signal sequence #status predicted <S>
F/161-182/Domain: transmembrane #status predicted <TM>
F/99,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

| | | | | |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match | 41.9%; | Score 471; | DB 2; | Length 218; |
| Best Local Similarity | 49.5%; | Pred. No. 3.6e-33; | | |

Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

[illegible]

```
QY      124 REFEEAHRDPVKTRRLPIRVTBAGEDPTSVSISIMTYLLVFLTWLLEIITYCRK 183
          || : | : ::| :|||::| :| :|||::|
DB      125 RLFPENYEHTSVKKIHIEVDKANRDASIVSEIMMYVLIVLTITWVAEMITYCYRK 184
```

```

Qy      184  VSKA-EEPAQENASDYLAIPSENKEN-SAVEEY 213
      ::| | | | | | | | | | | | | | | |
Db      185  IAAETETAQENASEYLAITSESKENCTGVQVAE 218

```

RESULT 4
MPRT0

myelin P0 protein precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2004
C.Accession: J00622; A22822
R.Lemke, G.; Lamar, E.; Patterson, J.
Neuron 1, 73-83, 1988
A.Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.
A.Reference number: J00622; MUID:90166482; PMID:2483091

A;Residues: 1-248 <LEM>
A;Cross-references: UNIPROT:P06907

R:Lemke, G.; Axel, R.
Cell 40, 501-508, 1985
A>Title: Isolation and sequence of a cDNA encoding the major structural protein of peripheral nervous system Schwann cells.
A:Reference number: A22822; MUID:85124601; PMID:2578885
A:Accession: A22822
A:Molecule type: mRNA
A:Residues: 1-248 <LEM2>
C:Comment: This protein is found only in peripheral nervous system Schwann cells.
C:Genetics:

A:introns: 23/1478/3; 150/1; 195/2; 215/3
 C:superfamily: myelin p0 protein; immunoglobulin homology
 C:keywords: glycoprotein; myelin; Schwann cell; structural
 F:1-39/Domain: signal sequence #status predicted <SIG>
 F:30-248/Product: myelin p0 protein #status predicted <MAT>
 F:30-153/Domain: extracellular #status predicted <ExD>
 F:43-129/Domain: immunoglobulin homology <IMM>
 F:154-176/Domain: transmembrane #status predicted <TMD>
 F:180-248/Domain: intracellular #status predicted <IND>

| | | | | |
|-----------------------|--------|--------------------|-------|----------------|
| Query Match | 15.6% | Score 175; | DB 1; | Length 248; |
| Best Local Similarity | 28.1%; | Pred. No. 1.1e-07; | | |
| Matches | 59; | Conservative | 34; | Mismatches 99; |
| | | | | Indels 18; |
| | | | | Gaps 7; |

0Y 1 ASULIATWMSVCEPCVCCEVSETEAAQGNPMKJCLISCKRBEVENTIVWEFIAKEGGK 70
0Y : : : : :
Db 20 SSLT-----SPLTAIVYTDRITYGAVGSVTLLHC-SFMSSSEVSDDISFTMRYPDEGR 74
0Y 71 DFL-IYYRRNGHOEVE--SPFOGLQMWSKDLDVSTIVLVNTLNDLSGLYCNSRREF 12

```

Db      75  DAISIFHYAKGQPYIDVEGTFKERRIQWGDPSWKDGSIVINHNLDYSDNGTFTCDVKNPDP 134
Oy      128  FEARHPVKTTRILIPRTVEAGDEFTSVSEIMYIILVLTMLLENI-YKRRVSK 166

```

```

D6      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
      135 -----IVGKTSQVLLYFEKVPRTYRGVLLGAVIGLIGVLLLLFYLRICWLRQA 198

OY      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
      187 AEE---AAQENASDYALIPSENKENSAPV 213

```

Db 189 ALQRLSAMEKGFHKSSKDDSSKRGRQTPV 218

RESULT 5

JH0252 myelin P0 protein precursor - human

N:Alternate names: myelin protein zero

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence revision 06-Dec-1996 #text_change 09-Jul-2004

C/Accession: JH0252; JN0704; I39378; I58118

R:Hayaoka, K.; Nanno, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uemura, K.

Biochem. Biophys. Res. Commun. 180, 515-518, 1991

A:Title: Isolation and sequence determination of cDNA encoding the major structural prot

A:Reference number: JH0252; MUID:92062068; PMID:1719967

A:Accession: JH0252

A:Molecule type: mRNA

A:Residues: 1-248 <RAY>

A:Cross-references: UNIPROT:P25189; GB:D10537; GB:D90501; NID:g220073; PIDN:BA01395.1;

A:Experimental source: fetus spinal cord

R:Hayaoka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Murai, Y.

Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993

A:Title: Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy type 1.

A:Reference number: JN0704; MUID:93356807; PMID:7688964

A:Accession: JN0704

A:Molecule type: mRNA

A:Residues: 1-248 <HA2>

R:Pham-Dinh, D.; Fourblin, Y.; Blanquet, F.; Mattei, M.G.; Roeckel, N.; Latour, P.; Chazot

Hum. Mol. Genet. 2, 2051-2054, 1993

A:Title: The major peripheral myelin protein zero gene: structure and localization in th

A:Reference number: I39378; MUID:94154677; PMID:7509228

A:Accession: I39378

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-248 <RES>

A:Cross-references: GB:I24893; NID:g454412; PIDN:AAA20656.1; PID:g529405

R:Kulkarni, T.; Bolhuis, P.A.; Wolterman, R.A.; Kemp, S.; de Nijenhuis, S.; Valentijn, L.

Nature Genet. 5, 35-39, 1993

A:Title: Deletion of the serine 34 codon from the major peripheral myelin protein P0 ge

A:Reference number: I58118; MUID:94035114; PMID:7693130

A:Accession: I58118

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-62, 64-115 <RB2>

A:Cross-references: GB:S66705; NID:g437048; PIDN:AA828708.1; PID:g437049

A:Experimental source: disease-state mutant

C:Comment: This protein, a small integral membrane glycoprotein, is the most abundant pr

C:Comment: This protein plays essential roles in both the elaboration and the subsequent

C:Genetics:

A:Gene: GDB:MP2; CMT1B; CMT1B; HMSNIB

A:Cross-references: GDB:125266; OMIM:159440

A:Map position: 1q22-1q23

A:Introns: 23/1, 78/3, 150/1, 195/2, 215/3

C:Superfamily: myelin P0 protein; immunoglobulin homology

C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein

F:1-29/Dominant: signal sequence #status predicted <SIG>

F:30-248/Product: peripheral myelin #status predicted <PER>

F:43-129/Dominant: immunoglobulin homology <IMM>

F:50-127/Dissulfide bonds: #status predicted

F:122/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 163.5; DB 1; Length 248;

Best Local Similarity 28.3%; Pred. No. 1e-06;

Matches 54; Conservative 33; Mismatches 81; Indels 23; Gaps 7;

Db 11 ASLVLYWVSCPPVCVEVSETEAVOQNPMLRCISCMKREVEATTVEWFRPEGCK 70

20 SSIVL-----SPAQIVVYDREHVGAVGSRVTLHC-SFMSSEWSDISFTWRYPGGR 74

71 DFLIYEYRNGHOVE--SPFOGRLOWNGSKLDQVSIPLVNTLNDSGLYTCNVSRFE 127

75 DAISIFHYAKGQYIDVGVGFKERIQWVGDPKMGDSIVHNDYSNGFTCDVKNPPD 134

128 FEARHPVKTTRLIPRLVTEAGEDTSVSEIMMYTLVFLMLIEMI-YCY----- 181

135 -----IVGTSQVTLVFEKVPFRYGVVLGAVIGVLVLLLLLFYVVRVCWMLRQA 188

RESULT 6

I38053 myelin protein zero - human

C:Species: Homo sapiens (man)

C>Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004

C/Accession: I38053; A49643; S43191

R:Rautenstrauss, B.; Nellis, E.; Gehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.

Hum. Mol. Genet. 3, 1701-1702, 1994

A:Title: Identification of a de novo insertional mutation in P0 in a patient with a Dejer

A:Reference number: I38053; MUID:9515435; PMID:7530550

A:Accession: I38053

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-251 <RES>

A:Cross-references: UNIPROT:Q14902; EMBL:Z31718; NID:g469516; PIDN:CAA83513.1; PID:g46951

R:Su, Y.; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.

Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993

A:Title: Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients.

A:Reference number: A49643; MUID:94068501; PMID:7504284

A:Accession: A49643

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 50-105 <SU1>

A:Experimental source: peripheral blood

C:Note: sequence extracted from NCBI backbone (NCBI:P:139777)

C:Genetics:

A:Gene: GDB:MP2; CMT1B; CMT1

A:Cross-references: GDB:125266; OMIM:159440

A:Map position: 1q22-1q23

C:Superfamily: myelin P0 protein; immunoglobulin homology

F:43-129/Dominant: immunoglobulin homology <IMM>

Query Match 14.5%; Score 163.5; DB 2; Length 251;

Best Local Similarity 28.3%; Pred. No. 1e-06;

Matches 54; Conservative 33; Mismatches 81; Indels 23; Gaps 7;

Db 11 ASLVLYWVSCPPVCVEVSETEAVOQNPMLRCISCMKREVEATTVEWFRPEGCK 70

20 SSIVL-----SPAQIVVYDREHVGAVGSRVTLHC-SFMSSEWSDISFTWRYPGGR 74

71 DFLIYEYRNGHOVE--SPFOGRLOWNGSKLDQVSIPLVNTLNDSGLYTCNVSRFE 127

75 DAISIFHYAKGQYIDVGVGFKERIQWVGDPKMGDSIVHNDYSNGFTCDVKNPPD 134

128 FEARHPVKTTRLIPRLVTEAGEDTSVSEIMMYTLVFLMLIEMI-YCY----- 181

135 -----IVGTSQVTLVFEKVPFRYGVVLGAVIGVLVLLLLLFYVVRVCWMLRQA 188

Query 182 ---RKVSKAE 189

Db 189 ALQRLSAMEK 199

RESULT 7

A29128 myelin P0 protein - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A29128

R:Sakamoto, Y.; Kitamura, K.; Yoshimura, K.; Nishijima, T.; Uemura, K.

J. Biol. Chem. 262, 4208-4214, 1987

A:Title: Complete amino acid sequence of P0 protein in bovine peripheral nerve myelin.

A:Reference number: A29128; MUID:8716035; PMID:2435734

A:Accession: A29128

A:Molecule type: protein

A:Residues: 1-219 <SAK>

A:Cross-references: UNIPROT:P10522

C:Superfamily: myelin P0 protein; immunoglobulin homology
C:Keywords: glycoprotein; membrane protein; myelin; phosphoprotein; Schwann cell; struct
F:14-100/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 159; DB 1; Length 219;
Best Local Similarity 26.5%; Pred. No. 2.2e-06;
Matches 52; Conservative 31; Mismatches 99; Indels 14; Gaps 6;

25 VCEVPSSEAEVQGNPMKLRCTSCMKREVEATVWEMYPEEGKDFL-ITYEYRNGQVE 83
1 IIVYTDKEVHGAVGSQVTLTYC-SFWSSEWSDLSFTWRQYDGGSDAIFHYAKGPY 59
84 VE--SPFOGRLQWNGSKDLQDVSTIVLNTLNDGLYTCNVSREFEFAHRPPVKTTRLI 141
60 IDEVGTFFKRIQWGDPRHKDGSIVIHNLVDYDNGFTCDVANNPD-----IVGKTSQV 113
142 PLRVTEAGEDFTSVSEIMMTILVFLTMLLMI-YCYRKVSKAEBA--AOENASD 197
114 TLVPEKVPTRRGVVLGAIVTGVLALLFLYIRCYMLRQAALQRLHAMEKGL 173
198 VLAISENKENSAVPV 213
174 HKTAKDASKRGKQTPV 189

RESULT 8

A54662
myelin P0 protein - mouse

C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C:Accession: A54662

R:You, K.H.; Hsieh, C.L.; Hayes, C.; Stahl, N.; Francke, U.; Popko, B.
Genomics 9, 751-757, 1991

A:Title: DNA sequence, genomic organization, and chromosomal localization of the mouse P
A:Reference number: A54662; MUID:91244320; PMID:1709914

A:Accession: A54662
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-247 <YOU>
A:Cross-references: GB:M62427

C:Superfamily: myelin P0 protein; immunoglobulin homology
F:43-128/Domain: immunoglobulin homology <IMM>

Query Match 13.7%; Score 154.5; DB 1; Length 247;
Best Local Similarity 27.6%; Pred. No. 6e-06;
Matches 58; Conservative 34; Mismatches 99; Indels 19; Gaps 8;

11 ASLVLIYVWVCFVCEVPSSEAEVQGNPMKLRCTSCMKREVEATVWEMYPEEGK 70
20 SSVLV-----SPALAIIVYTDREITGVAGVGSQVTLHC-SFWSSEWSDLSFTWRQY-EGGR 73
71 DPL-ITYEYRNGQVE--SPFOGRLQWNGSKDLQDVSTIVLNTLNDGLYTCNVSREFE 127
74 DAISIFHYAKGPYIDVGAFFKRIQWGDPRHKDGSIVIHNLVDYDNGFTCDVANNPD 133
128 FEHRPPVKTTRLIPLRVTEAGEDFTSVSEIMMTILVFLTMLLMI-YCYRKVSK 186
134 -----IVGKTSQVTLVPEKVPTRRGVVLGAIVTGVLALLFLYIRCYMLRQA 187
187 AEE--AAOENASDYLAIPESENKENSAVPV 213
188 ALQRLHAMEKGRFHKSKDSKRGKQTPV 217

RESULT 9

A32999
myelin P0 protein precursor - horn shark

C:Species: Heterodontus francisci (horn shark)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A32999

R:Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood,
J. Mol. Evol. 29, 149-156, 1989
A:Title: The myelin proteins of the shark brain are similar to the myelin proteins of th

A:Reference number: A32999; MUID:90040744; PMID:2478717

A:Accession: A32999
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-246 <SA>
A:Cross-references: UNIPROT:P20938; GB:X16714; NID:963976; PIDN:CB37865.1; PID:94467434

C:Superfamily: myelin P0 protein; immunoglobulin homology
C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
F:41-127/Domain: immunoglobulin homology <IMM>

Query Match 12.9%; Score 144.5; DB 1; Length 246;
Best Local Similarity 25.8%; Pred. No. 4.3e-05;
Matches 49; Conservative 37; Mismatches 77; Indels 27; Gaps 7;

16 IYWVSVCPVCEVPSSEAEVQGNPMKLRCTSCMKREVEATVWEMYPEFP 66
10 LFCSVLVAFSVLRPSQGISVSTHNLKHTVGSVTLTYC-GFWSSEYSDLTLSMRFP 68
67 EGKDFL-ITYEYRNGQVE--SPFOGRLQWNGSKDLQDVSTIVLNTLNDGLYTCNVS 123
69 DNSRDIISIFHYGNGVPYIEKMGQFRGVEWGDISKDGSIVIRNLDYINDGFTCDVK 128
124 REFEFAHRPPVKTTRLIPLRVTEAGEDFTSVSEIMMTILVFLTMLLMI 178
129 NPPD-----VVGTSDDVHLTVYDKIPVGAIVSGALITGFLIILVGLYL--FR 179
179 CYRKVSKAE 188
180 YVRRRANSE 189

RESULT 10

A61087
myelin P0 glycoprotein precursor - chicken

C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A61087

R:Barbu, M.
J. Neurosci. Res. 25, 143-151, 1990

A:Title: Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for earl
A:Reference number: A61087; MUID:90204597; PMID:1690817

A:Accession: A61087
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-249 <BAR>
A:Cross-references: UNIPROT:P37301

C:Comment: This protein is found only in peripheral nervous system Schwann cells.
C:Superfamily: myelin P0 protein; immunoglobulin homology

C:Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-249/Product: myelin P0 glycoprotein #status predicted <EXT>

F:30-153/Domain: extracellular #status predicted <EXT>
F:43-129/Domain: immunoglobulin homology <IMM>
F:154-179/Domain: transmembrane #status predicted <TM>
F:180-249/Domain: intracellular #status predicted <INT>

F:122/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 12.5%; Score 140.5; DB 1; Length 249;
Best Local Similarity 23.6%; Pred. No. 9.7e-05;
Matches 48; Conservative 43; Mismatches 87; Indels 25; Gaps 8;

13 IVLIIYVWVCFP-----VCEVPSSEAEVQGNPMKLRCTSCMKREVEATVWEMYPE 67
13 LILVGLLSASGSPSLIAHYTTPREVYGVTSHTLSC-SFWSSEWSEDSITYMHPAE 71
68 GKKDFL-ITYEYRNGQVE--SPFOGRLQWNGSKDLQDVSTIVLNTLNDGLYTCNVS 124
72 GSRDLSIFHYGKGPYIDVGSFEXKRMWGNRRKDGSIIVIHNLVDYDNGFTCDVK 131
125 EFEFAHRPPVKTTRLIPLRVTEAGEDFTSVSEIMMTILVFLTMLLMI-YCY-- 181
132 PPD-----IVGKSQVTLVYPEKVPTRRGVVLGAIVTGVLALLVALLVAVVLRFCWLR 185

Qy 182 -----RKVSKAEAA-AQENASD 197
 Db 186 ROAVLQRLRLSAMKGLQRSKD 208

RESULT 11

sodium channel beta 2 subunit - rat
 A:Accession: A57843
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: A57843
 R:isom, L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeek, R.E.; Reber, B.F.X.; Scheuer, Cell 83, 433-442, 1995
 A>Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein
 A:Reference number: A57843; PMID:96067641; PMID:8521473
 A:Accession: A57843
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-215 <RES>
 A:Cross-references: UNIPROT:P54900; EMBL:U37026; NID:g1086496; PIDN:AA052967.1; PID:g1086496
 A:Gene: SCN2B

Query Match 10.5%; Score 118; DB 2; Length 215;
 Best Local Similarity 25.1%; Pred. No. 0.007;
 Matches 49; Conservative 41; Mismatches 85; Indels 20; Gaps 8;

Qy 27 VEVPSSTEAQGNPMKRLCT--SCMKREVEATVWFFRPGG--KDFLIYFRNGH 81
 Db 32 VLVPTLLSVLNGSDTRLPCTFNSCYTVNHKQFS--LNMWYQECSCNCEWFLQFRMKIN 89
 Qy 82 QEVSPFOGRLOWNGSKDLDVSIITVNTLNDGLTCNVSRFEFEARFPVKTTRL 141
 Db 90 LKIER-FGDKVERFSGNPKYDVSVTLKNVQLEDEGIYNCYTV--PPDRHGHGK---I 142
 Qy 142 PLRVTEAGEDFTSVSEIMMYILLVFLTLMLEIMY-CYRKVSKAEAAQENASDYL 200
 Db 143 YLVQVLEVPERRSTVAIVIGASVGFLLAVIILVMVKVRR-----KEQKLTSTDLLK 197
 Qy 201 IPSENKENSAPVEE 215
 Db 198 TEEBCKTDEGNAED 212

RESULT 12

sodium channel beta 2 subunit - rat
 A:Accession: I61783
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I61783
 R:isom, L.L.; Ragsdale, D.S.; DeJonigh, K.S.; Westenhoeek, R.E.; Reber, B.F.X.; Scheuer, Cell 83, 433-442, 1995
 A>Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transmembrane Protein
 A:Reference number: A57843; PMID:96067641; PMID:8521473
 A:Accession: I61783
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-186 <RES>
 A:Cross-references: UNIPROT:Q62861; EMBL:U37147; NID:g1086498; PIDN:AA060506.1; PID:g1086498
 A:Gene: SCN2B
 A:introns: 50/3; 120/2

Query Match 10.4%; Score 117; DB 2; Length 186;
 Best Local Similarity 24.0%; Pred. No. 0.0073;
 Matches 49; Conservative 38; Mismatches 79; Indels 38; Gaps 8;

Qy 27 VEVPSSTEAQGNPMKRLCT--SCMKREVEATVWFFRPGGKDFLIYFRNGH 84
 Db 3 VLVPTLLSVLNGSDTRLPCTFNSCYTVNHKQFS--LNMWYQ-----ECSCNCEW 50
 Qy 85 ESPFO-----GRLOWNGSKDLDVSIITVNTLNDGLTCNVSRFEFEARH 132

Db 51 VLQFRMKIINLKLBERGDRVFSGNPSKYDVSVTLKNVQLEDEGIYNCYITN--PPDRHR 108
 Qy 133 PFVKTTRLPLRVTEAGEDFTSVSEIMMYILLVFLTLMLEIMY-CYRKVSKAEAA 191
 Db 109 GHGK---YLVQVLEVPERRSTVAIVIGASVGFLLAVIILVMVKVRR-----KKE 159
 Qy 192 QENASDYLAIIPSENKENSAPVEE 215
 Db 160 QKLTSTDLLKTEEBCKTDEGNAED 183

RESULT 13

fibroblast growth factor receptor - mouse
 A:Accession: S17295
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S17295
 R:Raz, V.; Kojima, Z.; Avivi, A.; Neufeld, G.; Givol, D.; Yarden, Y. Oncogene 6, 753-760, 1991
 A>Title: PCR-based identification of new receptors: molecular cloning of a receptor for fibroblast growth factor
 A:Reference number: S17295; PMID:91270892; PMID:1711190
 A:Accession: S17295
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-820 <RAZ>
 A:Cross-references: UNIPROT:P21803; EMBL:X55441; NID:g50141; PIDN:CAA39083.1; PID:g50142
 C:Superfamily: Basic fibroblast growth factor receptor 1; Immunoglobulin homology; protein F; 478-763/Domain: protein kinase homology <KIN>

Query Match 9.9%; Score 111.5; DB 2; Length 820;
 Best Local Similarity 25.9%; Pred. No. 0.11;
 Matches 41; Conservative 23; Mismatches 55; Indels 39; Gaps 7;

Qy 83 EYSPFOGRLOW-----NGSK-----DLQDVSIIVL---NVTLNDSC 116
 Db 278 KYVSDAQPHIQWIKHVKNGSKYGPDLPLKYLKKAAGVTTDKELVLRVTFPDAG 337
 Qy 117 LYTCNVSRFEFEARFPVKTTRLPLRVTE--EAGDFTSVSEIMMYILLVFLTLMLE 175
 Db 338 EYTCLAGNSIGISFHSAMV-TVLPAVREKEIRIASPDL---EIAIYCIQVGLIACMV 392
 Qy 176 EMIYCYRKVSKAEAAQENASDYLAIIPSENKENSAPVE 213
 Db 393 TVIFCRMKITTKK-----PDFSQPAVHKLTAKIPL 423

RESULT 14

fibroblast growth factor receptor bek precursor - mouse
 A:Accession: T1821 <MAN>
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1991 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: A44142; A31378
 R:Mansukhani, A.; Dell'Era, P.; Moscatelli, D.; Kornbluth, S.; Hanafusa, H.; Basilico, C. Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992
 A>Title: Characterization of the murine BEK fibroblast growth factor (FGF) receptor: act as a tyrosine kinase
 A:Reference number: A44142; PMID:92228773; PMID:1373495
 A:Accession: A44142
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
 A:Molecule type: mRNA
 A:Residues: 1-821 <MAN>
 A:Cross-references: UNIPROT:P21803; GB:M66441
 R:Kornbluth, S.; Paulson, K.E.; Hanafusa, H. Mol. Cell. Biol. 8, 5541-5544, 1988
 A>Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA
 A:Reference number: A31378; PMID:89219016; PMID:2468999
 A:Accession: A31378
 A:Molecule type: mRNA
 A:Residues: 477-821 <KOR>
 A:Cross-references: GB:M23362; NID:g533219; PIDN:AAA37285.1; PID:g533220
 C:Gene: FGFR3

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OM protein - protein search, using sw model

Run on: March 31, 2005, 20:02:27 ; Search time 116 seconds
(without alignments)
949.112 Million cell updates/sec

Title: US-09-977-579-2
Perfect score: 1124
Sequence: 1 MPFAFNRLPLASLVLYWVS.....SDYLAIPISENKENSAPVVE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1124 | 100.0 | 215 | 1 | CIB3_HUMAN |
| 2 | 1116 | 99.3 | 215 | 1 | CIB3_MACFA |
| 3 | 1105 | 98.3 | 215 | 1 | CIB3_RAT |
| 4 | 1097 | 97.6 | 215 | 1 | CIB3_MOUSE |
| 5 | 1097 | 97.6 | 268 | 2 | Q692Q3 |
| 6 | 714 | 63.5 | 215 | 2 | Q6DE47 |
| 7 | 477 | 42.4 | 218 | 1 | CIB1_RABIT |
| 8 | 472 | 42.0 | 218 | 1 | CIB1_RAT |
| 9 | 471 | 41.9 | 218 | 1 | CIB1_HUMAN |
| 10 | 468 | 41.6 | 218 | 1 | CIB1_MOUSE |
| 11 | 423 | 37.6 | 186 | 2 | Q8WU42 |
| 12 | 262.5 | 23.4 | 273 | 2 | Q9QXU3 |
| 13 | 258.5 | 23.0 | 268 | 2 | Q6TN97 |
| 14 | 208 | 18.5 | 66 | 2 | Q6LE66 |
| 15 | 178.5 | 15.9 | 203 | 2 | Q8JF66 |
| 16 | 172 | 15.6 | 248 | 1 | MYPO_RAT |
| 17 | 175 | 15.3 | 248 | 1 | MYPO_MOUSE |
| 18 | 163.5 | 14.5 | 209 | 2 | Q6DDH9 |
| 19 | 163.5 | 14.5 | 248 | 1 | MYPO_HUMAN |
| 20 | 163.5 | 14.5 | 251 | 2 | Q14902 |
| 21 | 161.5 | 14.4 | 248 | 2 | Q6WBS5 |
| 22 | 160.5 | 14.3 | 235 | 2 | Q6UW73 |
| 23 | 159 | 14.1 | 219 | 1 | MYPO_BOVIN |
| 24 | 155 | 13.8 | 215 | 2 | Q6NM73 |
| 25 | 150 | 13.3 | 202 | 2 | Q91406 |
| 26 | 149 | 13.3 | 215 | 1 | EVAI_MOUSE |
| 27 | 147 | 13.1 | 215 | 1 | EVAI_HUMAN |
| 28 | 147 | 13.1 | 215 | 2 | Q91W14 |
| 29 | 147 | 13.1 | 229 | 2 | Q8AWK3 |
| 30 | 144.5 | 12.9 | 246 | 1 | MYPO_HERPER |
| 31 | 140.5 | 12.5 | 249 | 1 | MYPO_CHICK |

| | | | | | | |
|----|-----|------|-----|---|----------|--------------------|
| 32 | 131 | 11.7 | 243 | 2 | Q9UE14 | Q9ue14 homo sapien |
| 33 | 131 | 11.7 | 269 | 2 | Q95297 | Q95297 homo sapien |
| 34 | 130 | 11.6 | 270 | 2 | Q6AYT8 | Q6ayt8 rattus norv |
| 35 | 127 | 11.3 | 183 | 2 | Q9UE16 | Q9ue16 homo sapien |
| 36 | 127 | 11.3 | 209 | 2 | Q9NYK4 | Q9nyk4 homo sapien |
| 37 | 125 | 11.1 | 199 | 2 | Q8JG36 | Q8jg36 brachydanio |
| 38 | 125 | 11.1 | 202 | 2 | Q8IX11 | Q8ix11 homo sapien |
| 39 | 125 | 11.1 | 209 | 2 | Q6GQX5 | Q6gqx5 mus musculu |
| 40 | 122 | 10.9 | 233 | 2 | Q8IX39 | Q8ix39 homo sapien |
| 41 | 121 | 10.8 | 287 | 2 | Q9D7B8 | Q9d7b8 mus musculu |
| 42 | 118 | 10.5 | 215 | 1 | CIB2_RAT | P54900 rattus norv |
| 43 | 118 | 10.5 | 287 | 2 | Q6SJF9 | Q6sjf9 mus musculu |
| 44 | 117 | 10.4 | 186 | 2 | Q62861 | Q62861 rattus norv |
| 45 | 116 | 10.3 | 222 | 2 | Q8IX38 | Q8ix38 homo sapien |

ALIGNMENTS

RESULT 1
CIB3_HUMAN STANDARD; PRT; 215 AA.
ID CIB3_HUMAN
AC Q9NY72; Q9ULR2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-3 subunit precursor.
GN Name=SCN3B; Synonyms=KIAA1158;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2010948; PubMed=10688874; DOI=10.1073/pnas.030362197;
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
RA Plincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;
RT "beta3: an additional auxiliary subunit of the voltage-sensitive
RT sodium channel that modulates channel gating with distinct kinetics.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gaessenhuber J., Glaesl S.,
RA Amsorge W., Boecker M., Bloecher H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Meuser H.-W., Oertzenaeft B., Obermaier B., Tampe J., Heubner D.,
RA Wamburt R., Korn B., Klein M., Pousheka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RN Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
CC -1- FUNCTION: Modulates channel kinetics. Causes unique
CC persistent sodium currents. Inactivates the sodium channel opening
CC slower than the beta-1 subunit. Its association with neurofascin
CC may target the sodium channels to the nodes of Ranvier of
CC developing axons and retain these channels at the nodes in mature
CC myelinated axons (By similarity).
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
CC noncovalently associated with alpha, while beta-2 is covalently
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate

with neurofascin (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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EMBL: AJ243396; CAB76825.1; -

EMBL: AL136589; CAB6524.1; -

EMBL: AB032984; BAA86472.1; ALT_INT.

HSSP: P06907; INEU.

GeneW: HGNC:20665; SCN3B.

H-InvDB: HIX0010216; -

MIM: 608214; -

GO: GO:0016021; C:integral to membrane; NAS.

GO: GO:0005248; F:voltage-gated sodium channel activity; NAS.

GO: GO:0006814; P:sodium ion transport; NAS.

InterPro: IPR007110; Ig-like.

PFam: PF00047; Ig_1.

PROSITE: PS50835; IG_LIKE; 1.

Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane; Voltage-gated channel.

SIGNAL 1 22

CHAIN 23 215

DOMAIN 23 159

TRANSMEM 160 180

DOMAIN 181 215

DISULFID 26 48

DISULFID 45 120

CARBOHYD 95 95

CARBOHYD 109 109

CARBOHYD 113 113

CARBOHYD 121 121

SEQUENCE 215 AA; 24702 MW; 70F6C604E9E26662 CRC64;

Query Match 100.0%; Score 1124; DB 1; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.le-93;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYVSVCFVCEVPESTEAQGNPKLRICSCMKREVEATTVV 60

DB 1 MPAFRLPLASLVLIYVSVCFVCEVPESTEAQGNPKLRICSCMKREVEATTVV 60

QY 61 EWFYRPEGGKDFLIYENRGHGVESPFQGRLOWNGSKDLDVSTIVLVNTLNDGLTYC 120

DB 61 EWFYRPEGGKDFLIYENRGHGVESPFQGRLOWNGSKDLDVSTIVLVNTLNDGLTYC 120

QY 121 NVSRREFEAPRPFKYKTRLLPLRTEAGDFTSVSEIMMYILVFLTLMLIEMTYC 180

DB 121 NVSRREFEAPRPFKYKTRLLPLRTEAGDFTSVSEIMMYILVFLTLMLIEMTYC 180

QY 181 YRKVSKAEAAQENASDYLAIPSENKENSAPVVEE 215

DB 181 YRKVSKAEAAQENASDYLAIPSENKENSAPVVEE 215

RESULT 2

CIB3_MACFA STANDARD; PRT; 215 AA.

QY Q8HXY7;

AC 29-MAR-2004 (rel. 43, Created)

DT 29-MAR-2004 (rel. 43, Last sequence update)

DT 25-OCT-2004 (rel. 45, Last annotation update)

DE Sodium channel beta-3 subunit precursor (Qmoa-13657).

GN Name=SCN3B;

OS Macaca fascicularis (Crap eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopitheciinae; Macaca.

NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Medulla oblongata;

RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Modulates channel gating kinetics. Causes unique persistent sodium currents. Inactivates the sodium channel opening slower than the beta-1 subunit. Its association with neurofascin may target the sodium channels to the nodes of Ranvier of developing axons and retain these channels at the nodes in mature myelinated axons (By similarity).

-1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion conducting pore forming alpha-subunit regulated by one or more beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are noncovalently associated with alpha, while beta-2 is covalently linked by disulfide bonds. Beta-1 or beta-3 subunits associate with neurofascin (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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EMBL: AB097521; BAC41746.1; -

HSSP: P06907; INEU.

InterPro: IPR007110; Ig-like.

PFam: PF00047; Ig_1.

PROSITE: PS50835; IG_LIKE; 1.

Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane; Voltage-gated channel.

SIGNAL 1 22

CHAIN 23 215

DOMAIN 23 159

TRANSMEM 160 180

DOMAIN 181 215

DISULFID 26 48

DISULFID 45 120

CARBOHYD 95 95

CARBOHYD 109 109

CARBOHYD 113 113

CARBOHYD 121 121

SEQUENCE 215 AA; 24702 MW; 25319D5ED218AACF CRC64;

Query Match 99.3%; Score 1116; DB 1; Length 215;

Best Local Similarity 99.1%; Pred. No. 6e-93; 2; Indels 0; Gaps 0;

Matches 213; Conservative 0; Mismatches 2;

QY 1 MPAFRLPLASLVLIYVSVCFVCEVPESTEAQGNPKLRICSCMKREVEATTVV 60

DB 1 MPAFRLPLASLVLIYVSVCFVCEVPESTEAQGNPKLRICSCMKREVEATTVV 60

QY 61 EWFYRPEGGKDFLIYENRGHGVESPFQGRLOWNGSKDLDVSTIVLVNTLNDGLTYC 120

DB 61 EWFYRPEGGKDFLIYENRGHGVESPFQGRLOWNGSKDLDVSTIVLVNTLNDGLTYC 120

QY 121 NVSRREFEAPRPFKYKTRLLPLRTEAGDFTSVSEIMMYILVFLTLMLIEMTYC 180

DB 121 NVSRREFEAPRPFKYKTRLLPLRTEAGDFTSVSEIMMYILVFLTLMLIEMTYC 180

QY 181 YRKVSKAEAAQENASDYLAIPSENKENSAPVVEE 215

DB 181 YRKVSKAEAAQENASDYLAIPSENKENSAPVVEE 215

RESULT 3
ID CIB3_RAT STANDARD; PRT; 215 AA.
AC 09J000;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-3 subunit precursor.
GN Name=Scn3b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND PROBABLE DISULFIDE BONDS.
RC TISSUE=Brain;
RX MEDLINE=20160948; PubMed=10688874; DOI=10.1073/pnas.030362197;
RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
RA Pincock R.D., Hynes J., Richardson P.J., Mizuguchi K., Jackson A.P.;
RT "Beta3: an additional auxiliary subunit of the voltage-sensitive
RT sodium channel that modulates channel gating with distinct kinetics.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).
RN [2]
RP SEQUENCE FROM N.A., CHARACTERIZATION, TISSUE SPECIFICITY, AND SUBUNIT.
RC STRAIN=Sprague-Dawley; TISSUE=Dorsal root ganglion;
RX MEDLINE=21919106; PubMed=11922146; DOI=10.1006/mcne.2001.1039;
RA Xu Y., Curtis R., Lawson D., Glibrid K., Ge P., Distefano P.S.,
RA Silos-Santiago I., Caterall W.A., Schener T.;
RT "Differential modulation of sodium channel gating and persistent
RT sodium currents by the beta1, beta2, and beta3 subunits.";
RL Mol. Cell. Neurosci. 18:570-580(2001).
RN [3]
RP INTERACTION WITH NEUROFASCIN
RX MEDLINE=21363577; PubMed=11470829; DOI=10.1083/jcb.200102086;
RA Ratcliffe C.F., Westbrock R.E., Curtis R., Caterall W.A.;
RT "Sodium channel beta1 and beta3 subunits associate with neurofascin
RT through their extracellular immunoglobulin-like domain.";
RL J. Cell Biol. 154:427-434(2001).
RN [4]
RP FUNCTION: Modulates channel gating kinetics. Causes unique
CC persistent sodium currents. Inactivates the sodium channel opening
CC slower than the beta-1 subunit. Its association with neurofascin
CC may target the sodium channels to the nodes of Ranvier of
CC myelinated axons and retain these channels at the nodes in mature
CC myelinated axons.
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
CC noncovalently associated with alpha, while beta-2 is covalently
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate
CC with neurofascin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed broadly in neurons in the central
CC and peripheral nervous systems, but not in glia and most
CC nonneuronal cells. Weak detection in lung and adrenal gland.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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CC
CC EMBL: AJ243395; CAB76838.1; -
CC EMBL: AF378093; AAK5415.1; -
CC HSSP: P06907; INEU
CC InterPro: IPR007110; Ig-like.
CC Pfam: PF00047; Ig_1.
CC PROSITE: PS50835; IG_LIKE_1.
KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
KW Signal; Sodium channel; Transmembrane; Voltage-gated channel.
FT SIGNAL 1 24 Potential.

FT CHAIN 25 215 Sodium channel beta-3 subunit.
FT DOMAIN 25 159 Extracellular (Potential).
FT TRANSMEM 160 180 Potential.
FT DOMAIN 181 215 Cytoplasmic (Potential).
FT DOMAIN 25 138 Ig-like C2-type.
FT DISULFID 26 48 Potential.
FT CARBOHYD 45 120 Potential.
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 215 AA; 24799 MW; 05684885E5AEF4F CRC64;

Query Match 98.3%; Score 1105; DB 1; Length 215;
Best Local Similarity 98.1%; Pred. No. 6e-92;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPANRLPLASLVLYWVSCPCVCEVSETEAVQGNPMKRCISCMREVEATTV 60
DB 1 MPANRLPLASLVLYWVSCPCVCEVSETEAVQGNPMKRCISCMREVEATTV 60
QY 61 EWFYRPGGKDFLIYERNGHGVESPFGRLQWNSKLDVSYTVANTLNDGLYTC 120
DB 61 EWFYRPGGKDFLIYERNGHGVESPFGRLQWNSKLDVSYTVANTLNDGLYTC 120
QY 121 NVSRPEPEAHKPFVKTTRLPLRTEBAGEDFTSVSEIMTYLTVLTLMIEMTYC 180
DB 121 NVSRPEPEAHKPFVKTTRLPLRTEBAGEDFTSVSEIMTYLTVLTLMIEMTYC 180
QY 181 YRKVSKAEBAQENASDYLAIPSENKNSAVPEE 215
DB 181 YRKVSKAEBAQENASDYLAIPSENKNSAVPEE 215

RESULT 4
ID CIB3_MOUSE STANDARD; PRT; 215 AA.
AC 08BH2; 091299;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel beta-3 subunit precursor.
GN Name=Scn3b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen C., Avery C., Kazen-Gillespie K., Isom L.L.;
RT "Mouse brain and heart beta 3 sodium channel cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi Y., Bono H., Kondo S.,
RA Nishida K., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gofjorth T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chottha C., Corbani L.E., Cousins S.,
RA Datta E., Dragani T.A., Fletcher C.F., Fortree A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurachkin I.V., Lee Y., Leinhard B., Lyons P.A.,
RA Magloct D.R., Maltchik L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilmig L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zevolan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakakura N., Sato K.,
RA Shiraki T., Maki K., Kawai U., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RT Nature 420:563-573 (2002).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain, and Olfactory epithelium;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Modulates channel gating kinetics. Causes unique
CC persistent sodium currents. Inactivates the sodium channel opening
CC slowlier than the beta-1 subunit. Its association with neurofascin
CC may target the sodium channels to the nodes of Ranvier of
CC developing axons and retain these channels at the nodes in mature
CC myelinated axons (By similarity).
CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
CC conducting pore forming alpha-subunit regulated by one or more
CC beta-1, beta-2 and/or beta-3 subunits. Beta-1 and beta-3 are
CC noncovalently associated with alpha, while beta-2 is covalently
CC linked by disulfide bonds. Beta-1 or beta-3 subunits associate
CC with neurofascin (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
CC EMBL, AY049036; AAL07512.1; -;
CC EMBL, AK049747; BAC33901.1; -;
CC EMBL, AK076466; BAC36356.1; -;
CC EMBL, BC053919; AAH53919.1; -;
CC EMBL, BC058636; AAH58636.1; -;
CC HSSP, P06907; INED.
CC MGD, MGI:1918882; Scn3b.
CC InterPro; IPR007110; Ig_1like.
CC Pfam; PF00047; Ig_1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
CC Signal; Sodium channel; Transmembrane; Voltage-gated channel.
CC SIGNAL 1 24
CC CHAIN 25 215 Sodium channel beta-3 subunit.

FT DOMAIN 25 159 Extracellular (Potential).
FT TRANSMEM 160 180 Potential.
FT DOMAIN 181 215 Cytoplasmic (Potential).
FT DOMAIN 25 138 Ig-like C2-type.
FT DISULFID 26 48 Potential.
FT DISULFID 45 120 Potential.
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 215 AA; 24789 MW; 0E07B47041784423 CRC64;

Query Match 97.6%; Score 1097; DB 1; Length 215;
Best Local Similarity 97.7%; Pred. No. 3.2e-91;
Matches 210; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPAFRLPLASLVLIYWSVCFVCPVSTTEAVQGNPKLRICSCMKREVEATTV 60
DB 1 MPAFRLPLASLVLIYWSVCFVCPVSTTEAVQGNPKLRICSCMKREVEATTV 60
QY 61 EHFYRPEGKDFLIYERNRGOEVSPFOGRLOMNGSKDLOVSTVLTNTLNDGSLYTC 120
DB 61 EHFYRPEGKDFLIYERNRGOEVSPFOGRLOMNGSKDLOVSTVLTNTLNDGSLYTC 120
QY 121 NVSRFEFEARHPFVKTRRLPLRVTEAGEDFTSVSEIMWYILVFTLMLIEMITC 180
DB 121 NVSRFEFEARHPFVKTRRLPLRVTEAGEDFTSVSEIMWYILVFTLMLIEMITC 180
QY 181 YRKVSKAEBAQENASDVLAISENKENSAYVEE 215
DB 181 YRKVSKAEBAQENASDVLAISENKENSAYVEE 215

RESULT 5
Q69ZQ3 PRELIMINARY; PRT; 268 AA.

AC Q69ZQ3;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MKIAA1158 protein (Fragment).
GN Name=MKIAA1158;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Suga Y., Seino S., Nishimura M., Katsuo T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologous of KIA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries";
RL DNA Res. 11:205-218 (2004).
DR EMBL; AK173115; BAD32393.1; -;
DR InterPro; IPR003599; Ig_1like.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
SQ SEQUENCE 268 AA; 30330 MW; 7A2655D5DD2409F CRC64;

Query Match 97.6%; Score 1097; DB 2; Length 268;
Best Local Similarity 97.7%; Pred. No. 4.1e-91;
Matches 210; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPAFRLPLASLVLIYWSVCFVCPVSTTEAVQGNPKLRICSCMKREVEATTV 60
|||||

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Db      54 MPAFNRLPLASVLVLYWVCPVCVEPSETEAVOGNSMKLRICISCMKREVEATTVV 113
Qy      61 EMFYRPGGKDFLIYERNGHOVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 120
Db      114 EMFYRPGGKDFLIYERNGHOVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 173
Qy      121 NVSRFEFEHARHPFKVTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLIEMITVC 180
Db      174 NVSRFEFEHARHPFKVTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLIEMITVC 233
Qy      181 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
Db      234 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 268

RESULT 6
ID      Q6DE47      PRELIMINARY;      PRT;      215 AA.
AC      Q6DE47;
DT      25-OCT-2004 (T-EMBLrel. 28, Created)
DT      25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE      Scn3b-prov protein.
GN      Name=scn3b-prov;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT      Richardson P.;
RT      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT      initiative.";
RT      Dev. Dyn. 225:384-391(2002).
RL      [2]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Klausner R.D., Collins F.S., Wagner L., Spemann C.M., Schlier G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datchenko L., Martinsina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Matra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL      [3]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      Klein S., Gerhard D.S.;
RT      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC077295; AAH77295.1; -.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00409; Ig_1.
DR      SMART; SM00406; IgV_1.

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DR      PROSITE; PS50835; IG LIKE; 1.
SQ      SEQUENCE 215 AA; 24472 MW; 2AAB890E46DE0289 CRC64;
Query Match 63.5%; Score 714; DB 2; Length 215;
Best Local Similarity 62.8%; Pred. No. 1.ee-56;
Matches 135; Conservative 32; Mismatches 48; Indels 0; Gaps 0;

Qy      1 MPAFNRLPLASVLVLYWVCPVCVEPSETEAVOGNSMKLRICISCMKREVEATTVV 60
Db      1 MAAMENIFWTDVSLFLMVFCSPCVCEVSGTEAVGEMNTLLCISCMKREVEATTVV 60
Qy      61 EMFYRPGGKDFLIYERNGHOVESPFQRLQWNSKDIQDVSIITVANTLNDGSLYTC 120
Db      61 RMFYQPDGGEILYERDGPDLIKSPLOQLQWNSKDIQDVSIITVANTLNDGSLYTC 120
Qy      121 NVSRFEFEHARHPFKVTRILPLRVTEAGEDFTSVSEIMMYILLVFLTMLIEMITVC 180
Db      121 HVARTLHFDHHRSTQSKSITLKWEAGEDFTSVSKIMMYILLVFLTMLIEMITVC 180
Qy      181 YRKVSKAEAAQENASDYLAIPSENKENSAPVEE 215
Db      181 YRKISKAEVYQESVTDYLAIPSENKENSAPVEE 215

RESULT 7
ID      CIB1_RABIT      STANDARD;      PRT;      218 AA.
AC      P53788;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Sodium channel beta-1 subunit precursor.
GN      Name=SCN1B;
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=New Zealand white; TISSUE=Sciatic nerve;
RX      MEDLINE=96235151; PubMed=8666261; DOI=10.1016/0378-1119(95)00871-3;
RA      Belcher S.M., Howe J.R.;
RT      "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
RT      rabbit.";
RL      Gene 170:285-286(1996).
RN      -1- FUNCTION: Crucial in the assembly, expression, and functional
RN      modulation of the heterotrimeric complex of the sodium channel.
RN      The beta-1 subunit can modulate multiple alpha subunit isoforms
RN      from brain, skeletal muscle, and heart. Its association with
RN      neurofascin may target the sodium channels to the nodes of Ranvier
RN      of developing axons and retain these channels at the nodes in
RN      mature myelinated axons (By similarity).
RN      -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
RN      conducting pore forming alpha-subunit regulated by one or more
RN      beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
RN      associated with alpha, while beta-2 is covalently linked by
RN      disulfide bonds. Beta-1 or beta-3 subunits associate with
RN      neurofascin (By similarity).
RN      -1- SUBCELLULAR LOCATION: Type I membrane protein.
RN      -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; J03382; AAB17572.1; -.
DR      PIR; JC4788; JC4788.
DR      InterPro; IPR007110; Ig-like.
DR      Pfam; PF00047; Ig_1.

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DR PROSITE; P550835; IG LIKE; FALSE NEG.
 KW Glycoprotein; Immunoglobulin domain; Ion transport; Ionic channel;
 KM Signal; Sodium channel; Transmembrane; Voltage-gated channel.
 FT SIGNAL 1 18 By similarity, beta-1 subunit.
 FT CHAIN 19 218 Sodium channel (Potential).
 FT DOMAIN 19 160 Extracellular (Potential).
 FT TRANSMEM 161 182 Potential.
 FT DOMAIN 183 218 Cytoplasmic (Potential).
 FT DOMAIN 22 150 Ig-like C2-type.
 FT DISULFID 21 43 Potential.
 FT DISULFID 40 121 Potential.
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 218 AA; 24706 MW; 39BD174E1FAE7FD2 CRC64;

Query Match 42.4%; Score 477; DB 1; Length 218;
 Best Local Similarity 49.5%; Pred. No. 4,6e-35;
 Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;

OY 10 LASLVLIYVWSYCFVCEVPESETAVOQNPMLKRCISCKRKEVEATTVVEMFYRPEGG 69
 DB 5 LAFVVGALVSSAWGCVDETEAVYGMTEFKLICISCKRSEETAEFTETWTRQKGT 64
 OY 70 KDFL-IYEVYRNHGOVESP--FOGRLQWNGS---KDLQDVSTVLTNLTNDGLTYCNVS 123
 DB 65 BEFVKILRYENEVLDLEDEREPEGVWNGSGTDLQDLSTFINVTVNHSQDYQCHYV 124
 OY 124 REFEFARPPVKTTRLPLRVTBEAGDFTSVSEIMMYILVPLTLMLEIMTYCYRK 183
 DB 125 RLSEFENEHNTSVYKKTILHEVDKANDRMASIVSEIMMYILVPLTLMLEIMTYCYRK 184
 OY 184 VSKA-EFAAQAENASDYLAIPSENKEN-SAPVPEE 215
 DB 185 IAAATEAAQAENASEYLAIITSSKENCTGVQVAE 218

RESULT 8
 ID CIB1_RAT STANDARD; PRT; 218 AA.
 AC Q00954;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 GN Name=Scn1b;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RA MEDLINE=9227107; PubMed=1375395;
 RA Isom L.L., De Jongh K.S., Patton D.E., Reber B.F.X., Offord J.,
 RA Charbonneau H., Walsh K., Goldin A.L., Catterall W.A.;
 RT "Primary structure and functional expression of the beta 1 subunit of
 RT the rat brain sodium channel.";
 RL Science 256:839-842(1992).
 RN [2]
 RP INTERACTION WITH NEUROFASCIN.
 RX MEDLINE=2136357; PubMed=11470829; DOI=10.1083/jcb.200102086;
 RA Ratcliffe C.F., Westenbroek R.E., Curtis R., Catterall W.A.;
 RT "Sodium channel beta1 and beta3 subunits associate with neurofascin
 RT through their extracellular immunoglobulin-like domain.";
 RL J. Cell Biol. 154:427-434(2001).
 CC -!- FUNCTION: Crucial in the assembly, expression, and functional
 CC modulation of the heterotrimeric complex of the sodium isoforms
 CC the beta-1 subunit can modulate multiple alpha subunit isoforms
 CC from brain, skeletal muscle, and heart. Its association with
 CC neurofascin may target the sodium channels to the nodes of Ranvier
 CC of developing axons and retain these channels at the nodes in

CC mature myelinated axons.
 CC -!- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 CC conducting pore forming alpha-subunit regulated by one or more
 CC beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
 CC associated with alpha, while beta-2 is covalently linked by
 CC disulfide bonds. Beta-1 or beta-3 subunits associate with
 CC neurofascin.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in brain, heart, skeletal muscle and
 CC spinal cord.
 CC -!- DEVELOPMENTAL STAGE: In developing nodes of Ranvier, it is
 CC localized in the sciatic nerve at postnatal days 3 and 10, during
 CC the process of myelination and maturation of the nodes.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 CC EMBL; M91808; AAA8513.1; -.
 DR PIR; A42737; A42737.
 DR RGD; 3631; Scn1b.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_1.
 DR PROSITE; P550835; IG LIKE; FALSE NEG.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT SIGNAL 1 18 Sodium channel beta-1 subunit.
 FT CHAIN 19 218 Extracellular (Potential).
 FT DOMAIN 19 160 Potential.
 FT TRANSMEM 161 182 Cytoplasmic (Potential).
 FT DOMAIN 183 218 Potential.
 FT DOMAIN 22 150 Ig-like C2-type.
 FT DISULFID 21 43 Potential.
 FT DISULFID 40 121 Potential.
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 218 AA; 24692 MW; 0BA84FC44FF2306B CRC64;

Query Match 42.0%; Score 472; DB 1; Length 218;
 Best Local Similarity 49.1%; Pred. No. 1.3e-34;
 Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;

OY 10 LASLVLIYVWSYCFVCEVPESETAVOQNPMLKRCISCKRKEVEATTVVEMFYRPEGG 69
 DB 5 LAFVVGALVSSAWGCVDETEAVYGMTEFKLICISCKRSEETAEFTETWTRQKGT 64
 OY 70 KDFL-IYEVYRNHGOVESP--FOGRLQWNGS---KDLQDVSTVLTNLTNDGLTYCNVS 123
 DB 65 BEFVKILRYENEVLDLEDEREPEGVWNGSGTDLQDLSTFINVTVNHSQDYQCHYV 124
 OY 124 REFEFARPPVKTTRLPLRVTBEAGDFTSVSEIMMYILVPLTLMLEIMTYCYRK 183
 DB 125 RLSEFENEHNTSVYKKTILHEVDKANDRMASIVSEIMMYILVPLTLMLEIMTYCYRK 184
 OY 184 VSKA-EFAAQAENASDYLAIPSENKEN-SAPVPEE 215
 DB 185 IAAATEAAQAENASEYLAIITSSKENCTGVQVAE 218

RESULT 9
 ID CIB1_HUMAN STANDARD; PRT; 218 AA.
 AC Q07699;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

05-JUL-2004 (Rel. 44, last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 GN Name=SCN1B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93357746; PubMed=8394762;
 RA McClatchey A.I., Cannon S.C., Staugenhardt S.A., Guseella J.F.;
 RT "The cloning and expression of a sodium channel beta 1-subunit cDNA
 from human brain.";
 RL Hum. Mol. Genet. 2:745-749(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart, and Skeletal muscle;
 RX MEDLINE=94171787; PubMed=8125980;
 RA Makita N., Bennett P.B. Jr., George A.L. Jr.;
 RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult
 human skeletal muscle, heart, and brain is encoded by a single gene.";
 RL J. Biol. Chem. 269:7571-7578(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95154833; PubMed=7851891;
 RA Makita N., Sloan-Brown K., Weghuis D.O., Rogers H.-H.,
 George A.L. Jr.;
 RT "Genomic organization and chromosomal assignment of the human voltage-
 gated Na+ channel beta 1 subunit gene (SCN1B).";
 RL Genomics 23:628-634(1994).
 RN [4]
 RP VARIANT GEF5+ TRP-121.
 RX MEDLINE=98361163; PubMed=9697698; DOI=10.1038/1252;
 RA Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr.,
 Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R.,
 Berkovic S.F., Mulley J.C.;
 RT "Rebrite seizures and generalized epilepsy associated with a mutation
 in the Na(+)-channel beta-1 subunit gene SCN1B.";
 RL Nat. Genet. 19:366-370(1998).
 CC -1- FUNCTION: Crucial in the assembly, expression, and functional
 modulation of the heterotrimeric complex of the sodium channel.
 CC The beta-1 subunit can modulate multiple alpha subunit isoforms
 from brain, skeletal muscle, and heart. Its association with
 neurofascin may target the sodium channels to the nodes of Ranvier
 of developing axons and retain these channels at the nodes in
 mature myelinated axons.
 CC -1- SUBUNIT: The voltage-sensitive sodium channel consists of an ion
 conducting pore forming alpha-subunit regulated by one or more
 beta-1, beta-2 and beta-3. Beta-1 and beta-3 are noncovalently
 associated with alpha, while beta-2 is covalently linked by
 disulfide bonds. Beta-1 or beta-3 subunits associate with
 neurofascin.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, heart
 and brain.
 CC -1- DISEASE: Defects in SCN1B are a cause of generalized epilepsy with
 febrile seizures plus (GEFS+) [MIM:604233]. GEFS+ is a disease
 characterized by a highly variable phenotype combining febrile
 seizures, generalized seizures often precipitated by fever at age
 6 years or more, and partial seizures, with a variable degree of
 severity.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).

DR EMBL; L10338; AAA60391.1; -;
 DR EMBL; L16242; AAA61277.1; -;
 DR EMBL; U12193; AAB97608.1; -;
 DR EMBL; U12189; AAB97608.1; JOINED.
 DR EMBL; U12190; AAB97608.1; JOINED.
 DR EMBL; U12191; AAB97608.1; JOINED.
 DR EMBL; U12192; AAB97608.1; JOINED.
 DR PIR; A55734; A55734.
 DR Genew; HGNC:10586; SCN1B.
 DR MIM; 600235; -;
 DR MIM; 604233; -;
 DR GO; GO:0005248; F: voltage-gated sodium channel activity; TAS.
 DR GO; GO:0006814; P: sodium ion transport; TAS.
 DR GO; GO:0007268; P: synaptic transmission; TAS.
 DR InterPro; IPR007110; 1g-like.
 DR Pfam; PF00047; 1g; 1.
 DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
 KW Disease mutation; Epilepsy; Glycoprotein; Immunoglobulin domain;
 KW Ion transport; Ionic channel; Signal; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT SIGNAL 1 18
 FT CHAIN 19 218
 FT DOMAIN 19 160
 FT TRANSMEM 161 182
 FT DOMAIN 183 218
 FT DOMAIN 22 150
 FT DISULFID 21 43
 FT CARBOHYD 93 93
 FT CARBOHYD 110 110
 FT CARBOHYD 114 114
 FT CARBOHYD 135 135
 FT VARIANT 121 121
 FT C->W (in GEFS+).
 FT /FTID=VAR_010165.
 SQ SEQUENCE 218 AA; 24707 MW; 09B812FA3F9E9018 CRC64;
 Query Match 41.9%; Score 471; DB 1; Length 218;
 Best Local Similarity 49.5%; Pred. No. 1.6e-34;
 Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;
 QY 10 LASLVLIYVWSVCFPVCEVPEVSETEAVQGNPKLRCSCKMKREVEATVWEPYREGG 69
 DB 5 LALVVGALVSSACGCEVDESETEAVYGMTPILICISCRSRSTNAETETWFRQGT 64
 QY 70 KDFL-IYEYNGHQEVSP--FGRLQWNGS---KDLQVSYIVLVNTLNDGLTYCNVS 123
 DB 65 EEFVKILRYENEVLQLEDEDERFEGRVVWNGSRGKDLQDLSIFITVNTYHSGDYECHVY 124
 QY 124 REEFPEAHRFVVTTRLIPRLVTEBEAGDEFTSVSEIMTYILVFLTMLIEMTYCYRK 183
 DB 125 RLIFPEYEHNTSVVKKIHLEVDKARDMASTVSEIMTYILVFLTMLVEMTYCYRK 184
 QY 184 VSKA-EEAAQENASDYLAIPSENKEN-SAVPEE 215
 DB 185 IAAATETPAQENASEYLAITSEKENCTGVQVAE 218
 RESULT 10
 CIB1 MOUSE
 ID CIB1 MOUSE STANDARD; PRT; 218 AA.
 AC P97952;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 GN Name=Scn1b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC021266; AAH21266.2; -

DR Pfam; PF00047; 1g; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1

SO SEQUENCE 186 AA; 21554 MW; A7DAEF7E75FACF00 CRC64;

Query Match 37.6%; Score 423; DB 2; Length 186;

Best Local Similarity 48.9%; Pred. No. 3e-30;

Matches 91; Conservative 30; Mismatches 57; Indels 8; Gaps 5;

QY 38 GNPWKRCISCKREEVEATVVEWFRPGKDFL-IEYRNHGOVESP--FOGRLQW 94

DB 1 GMFTKILCISCKRSENAETFTETFRQKTEEFVKILRYENVQLQEDEREGRVVW 60

QY 95 NGS---KDLQDVSTVANTLNDGLTYCNVSRFEFEARPPVKTTRLPLRYTEAGE 151

DB 61 NGSRGTKDLDLSFTINVTYHNSGDYCHVYRLFFENEHNTSVVKKIIEVVDRNR 120

QY 152 DFTSVSEIMWYILVFLTLMLIEMTYCYKYSKA-EBAAGNADSYLAIPSENKEN-S 209

DB 121 DAMSISEIMWYILVFLTLMLIEMTYCYKYSKA-EBAAGNADSYLAIPSENKEN-S 180

QY 210 AVPEVE 215

DB 181 GVOVAE 186

RESULT 12

Q9OXU3 PRELIMINARY; PRT; 273 AA.

ID 09OXU3

AC 09OXU3

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Voltage-gated sodium channel subunit beta1-A.

GN Name=SCN1B;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN SEQUENCE FROM N.A.

RP MEDLINE=20092877; PubMed=10625649; DOI=10.1074/jbc.275.2.1079;

RA Kazen-Gillespie K.A., Ragsdale D.S., D'Andrea M.R., Mattei L.N.,

RT "Cloning, localization, and functional expression of sodium channel

beta1A subunit."

RL J. Biol. Chem. 275.1079-1088(2000).

DR EMBL; AF182849; AAR25186.1; -

DR GO; GO:0005216; F:ion channel activity; IEA.

DR InterPro; IPR007110; IG-1like.

DR Pfam; PF00047; 1g; 1.

KW Ionic channel.

SO SEQUENCE 273 AA; 31063 MW; 156A31899A906849 CRC64;

Query Match 23.4%; Score 262.5; DB 2; Length 273;

Best Local Similarity 39.3%; Pred. No. 1.6e-15;

Matches 68; Conservative 23; Mismatches 53; Indels 29; Gaps 5;

QY 10 LALVLIWVSCPEPVCVEPSETEAVQGNPKLRCSCKRREVEATVVEWFRPEG 69

DB 5 LALVGAALVSSAGCGVEVDSETEAVYGMFTKILCISCKRSENAETFTETFRQKGT 64

QY 70 KDFL-IEYRNHGOVESP--FOGRLQWNGS---KDLQDVSTVANTLNDGLTYCNVS 123

DB 65 EEFVKILRYENVQLQEDEREGRVVWNSRGTKDLDLSFTINVTYHNSGDYCHVY 124

QY 124 REFEFEARPPVKTTRLPLRYTEAGEFTSVSEIMWYIL---LVPLTLW 172

DB 125 RLFFFDNY-----EHNTSVVKKIIEVVDRNR 158

RESULT 13

O6TN97

AC O6TN97

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Voltage gated sodium channel beta1b subunit.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.

RP MEDLINE=22985127; PubMed=14622265;

RA Qin N., D'Andrea M.R., Lubin M.U., Shafae N., Codd E.E., Correa A.M.;

RT "Molecular cloning and functional expression of the human sodium

channel beta1b subunit, a novel splicing variant of the beta1

subunit."

RL Eur. J. Biochem. 270.4762-4770(2003).

DR EMBL; AY391842; AAR25552.1; -

DR GO; GO:0005216; F:ion channel activity; IEA.

DR InterPro; IPR007110; IG-1like.

DR Pfam; PF00047; 1g; 1.

KW Ionic channel.

SO SEQUENCE 268 AA; 30440 MW; D9A001E676C0FAD1 CRC64;

Query Match 23.0%; Score 258.5; DB 2; Length 268;

Best Local Similarity 43.2%; Pred. No. 3.6e-15;

Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 10 LALVLIWVSCPEPVCVEPSETEAVQGNPKLRCSCKRREVEATVVEWFRPEG 69

DB 5 LALVGAALVSSAGCGVEVDSETEAVYGMFTKILCISCKRSENAETFTETFRQKGT 64

QY 70 KDFL-IEYRNHGOVESP--FOGRLQWNGS---KDLQDVSTVANTLNDGLTYCNVS 123

DB 65 EEFVKILRYENVQLQEDEREGRVVWNSRGTKDLDLSFTINVTYHNSGDYCHVY 124

QY 124 REFEFEARPPVKTTRLPLRYTEAGE 151

DB 125 RLFFFDNY-----EHNTSVVKKIIEVVDRNR 151

RESULT 14

O6LE66

AC O6LE66

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Voltage-dependent Na+ channel beta-1 subunit (Fragment).

GN Name=beta 1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN SEQUENCE FROM N.A.

RP MEDLINE=96140573; PubMed=8549781; DOI=10.1016/0014-5793(95)01400-4;

RA Dib-Hajj S.D., Waxman S.G.;

RT "Genes encoding the beta 1 subunit of voltage-dependent Na+ channel in

rat, mouse and human contain conserved introns."

RL FEBS Lett. 377.485-488(1995).

RN TISSUE=Liver;

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

MDLINE=92271207; PubMed=1375395;

RA Isom L.L., De Jongh K.S., Patton D.E., Reber B.F., Offord J.,

RT Charbonneau H., Walsh K., Goldin A.L., Caterall W.A.;

RT "Primary structure and functional expression of the beta 1 subunit of

the rat brain sodium channel."

RL Science 256:839-842(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95024086; PubMed=7937931;
RA Oh Y., Waxman S.G.;
RT "The beta 1 subunit mRNA of the rat brain Na+ channel is expressed in glial cells."
RL Proc. Natl. Acad. Sci. U.S.A. 91:9985-9989(1994).
DR EMBL: L48688; AAB02428.1; -
DR GO: GO:0005216; F-100 channel activity; IEA.
KM Tonic channel.
FT NON_TER
SQ SEQUENCE 66 AA; 7208 MW; 4DB598740914D95B CRC64;

Query Match 18.5%; Score 208; DB 2; Length 66;
Best Local Similarity 63.6%; Pred. No. 2.8e-11;
Matches 42; Conservative 12; Mismatches 10; Indels 2; Gaps 2;

QY 152 DFTSVSEIMMYLIVFLTLMLIMYCYRKYSKA-EEAQAENASDYLAIPSENKEN-S 209
DB 1 DWASIVSEIMMYLIVFLTLMLIMYCYRKYSKA-EEAQAENASDYLAIPSENKEN-S 60

QY 210 AVPEE 215
DB 61 GVOVAE 66

RESULT 15

Q8JFG6 PRELIMINARY; PRT; 203 AA.

AC Q8JFG6;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Myelin protein zero.
GN Name=mpz;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myelin;
RA Schweitzer J., Becker T., Becker C.G., Schachner M.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSj databases.
DR EMBL: AJ489219; CAD32961.1; -.
DR HSP; P06907; INED.
DR ZFIN; ZDB-GENE-010724-4; mpz.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 203 AA; 22097 MW; 12614E9076D373D1 CRC64;

Query Match 15.9%; Score 178.5; DB 2; Length 203;
Best Local Similarity 26.9%; Pred. No. 4.6e-08;
Matches 53; Conservative 41; Mismatches 86; Indels 17; Gaps 7;

QY 10 LASTLIVVSVCFPCVSEVSETEAVQGNPKLRICSCMKREVEATVVEWFFRPEG 69
DB 7 LTVSVLLGIASQSTALVAVTDEKHALVGSVLRISC-SFESWQWTSPEVSTWHRYPDGA 65

QY 70 KDPL-IVERYNG--HOEVSPFCGRLOWNGSKLDVSIIVNLVTLNDGLTYCNVSRF 126
DB 66 KDAISIFHGGGEAVPANRGPQNRLFFVGNPSRDSILIKNLDPGNDGFTCDAKNPP 125

QY 127 EFAEARPPVKTTRLPL-RVTEAGEDFTSVSEIMMYLIV---FLTLMLIMYIC- 180
DB 127 EFAEARPPVKTTRLPL-RVTEAGEDFTSVSEIMMYLIV---FLTLMLIMYIC- 180

DB 126 DIGH---PSTIRLLVEKVPVQAGVITGSIIGVVLGLLIIVAIYYIMRFLVARRVPSL 182
QY 181 ----YRKVSKAEBAQE 193
DB 183 SMSKHGKKKGKSGSQ 199

Search completed: March 31, 2005, 20:21:50
Job time : 117 secs


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DB 241 GGCCTTCCTCGGTGAGAAAGTCGCCCTGGGGGCGAGTTCCTCCAAAGGGTTCCTCG 300
QY 301 AAGAGATCTGAGAGGGGCGAGTCCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAAAC 360
DB 301 AAGAGATCTGAGAGGGGCGAGTCCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAAAC 360
QY 361 CGCCAGCCCCAGAGATGCTGCTTCATTAATTTGTTCCCTGGCTTCTCTCGTCT 420
DB 361 CGCCAGCCCCAGAGATGCTGCTTCATTAATTTGTTCCCTGGCTTCTCTCGTCT 420
QY 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGTGAAGTGCCTCGAGACGAGGCC 480
DB 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGTGAAGTGCCTCGAGACGAGGCC 480
QY 481 GTGCGAGGGGAACCCCACTGAAGCTGCGCTGCATCTCTCGATGAAGAAGAGAGAGGTGAG 540
DB 481 GTGCGAGGGGAACCCCACTGAAGCTGCGCTGCATCTCTCGATGAAGAAGAGAGAGGTGAG 540
QY 541 GCCACCAACGCTGGTGAATGTTCTACAGGCGCGAGGGCGGTAAAGATTCTTAATTAC 600
DB 541 GCCACCAACGCTGGTGAATGTTCTACAGGCGCGAGGGCGGTAAAGATTCTTAATTAC 600
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DB 781 AAGAGCAGCGGCTGATCCCTTAAAGAGTACCGAGAGGCTGAGAGAGACTTCACTCT 840
QY 841 GGTGTCTGAGAAATCATGATGTACATCCTGTGTGTCTTCAACCTGTGTGTGTGTGTGT 900
DB 841 GGTGTCTGAGAAATCATGATGTACATCCTGTGTGTCTTCAACCTGTGTGTGTGTGTGT 900
QY 901 GAGATGATATATTGTCTACAGAAAGGTCTCAAAAAGCCGAGAGAGGAGCCCAAGAAACGG 960
DB 901 GAGATGATATATTGTCTACAGAAAGGTCTCAAAAAGCCGAGAGAGGAGCCCAAGAAACGG 960
QY 961 TCTGACTACCTTGGCCATCTGAGAACTGAGGAACTGTGCGGTACAGTGGAGAA 1020
DB 961 TCTGACTACCTTGGCCATCTGAGAACTGAGGAACTGTGCGGTACAGTGGAGAA 1020
QY 1021 TGAACAAGAGAGAGTGTGATGAGAGTGGCTGAAACACTGAGGAGATGAGATCCCATG 1080
DB 1021 TGAACAAGAGAGAGTGTGATGAGAGTGGCTGAAACACTGAGGAGATGAGATCCCATG 1080
QY 1081 TTCAAGCAATGCAATGAGCATGAGAGGGGCGCCCAAGGGGCCCATGCTTCCCTTCATGC 1140
DB 1081 TTCAAGCAATGCAATGAGCATGAGAGGGGCGCCCAAGGGGCCCATGCTTCCCTTCATGC 1140
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DB 1141 ATTCATTTGTTCTGTTCAATTCATTCATCAATCAATCAATCAATCAATCAATCAATCT 1200
QY 1201 GACTCCCTTAATCTCAACAGACCTTACAGCAACATTAAGACTTTCAGAACTGAGAAAGCCG 1260
DB 1201 GACTCCCTTAATCTCAACAGACCTTACAGCAACATTAAGACTTTCAGAACTGAGAAAGCCG 1260
QY 1261 G 1261
DB 1261 G 1261
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RESULT 2

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AX039100
LOCUS AX039100 1261 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 4 from Patent WO0063367.
ACCESSION AX039100
VERSION AX039100.1 GI:11229276
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Cox,P., Dixon,A., Jackson,A. and Morgan,K.
A novel family of beta sub-unit proteins from a voltage-gated sodi
um channel, nucleic acids encoding them and therapeutic or
diagnostic uses thereof
Patent: WO 0063367-A 4 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical
Services Limited (GB)
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 VERSION AJ243396.2 GI:7242612
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Pinnock, R.D., Hynes, J., Richardson, P.J., Mizunuchi, K. and Jackson, A.P.
 TITLE beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
 MEDLINE 20160948
 PUBMED 10688874
 REFERENCE 2 Morgan, K.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
 REMARK Revised by [4]
 REFERENCE 3 (bases 1 to 1261)

AUTHORS Morgan, K.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
 COMMENT On Mar 14, 2000 this sequence version replaced gi:7160974.
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| VERSION | AB032984.1 | GI:6330135 | | |
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| SOURCE | | | | |
| ORGANISM | Homo sapiens (human) | | | |
| REFERENCE | | | | |
| AUTHORS | Mukoyama,M., Negase,T., Ishikawa,K., Kikuno,R., Nomura,N. and Ohara,O. | | | |
| TITLE | Characterization of cDNA clones selected by the Genemark analysis from size-fractionated cDNA libraries from human Brain | | | |
| JOURNAL | DNA Res. 6 (5), 329-336 (1999) | | | |
| MEDLINE | 20039618 | | | |
| PUBMED | 10574461 | | | |
| REFERENCE | 2 (bases 1 to 5306) | | | |

AUTHORS
TITLE
JOURNAL

Direct Submission
Submitted (04-OCT-1996) Osamu Chiba, Kazusa DNA Research Institute
Laboratory of DNA Technology, 1332, Yata, Kikarazu, Chiba
292-0812, Japan (E-mail:chiba@kzusa.or.jp,
URL: <http://www.kazusa.or.jp/huge/>, Tel: +81-438-52-3913,
fax: +81-438-52-3914)

FEATURES

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| LOCUS | | | | |
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| VERSION | | AB097521.1 | GI:26449236 | |
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| SOURCE | | | Macaca fascicularis (crab-eating macaque) | |
| ORGANISM | | | Macaca fascicularis | |
| | | | Eumalota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarcharia; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca. | |
| REFERENCE | | | | |
| AUTHORS | | | Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M., Suto,Y., Hirai,M., Terzo,K., Suzuki,Y., Sugano,S. and Hashimoto,K. | |
| TITLE | | | Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes | |
| JOURNAL | | | Gene 275 (1), 31-37 (2001) | |
| MEDLINE | | | 21458551 | |
| PUBMED | | | 11574149 | |
| REFERENCE | | | 2 (bases 1 to 3296) | |
| AUTHORS | | | Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S. | |
| TITLE | | | Direct Submission | |
| JOURNAL | | | Submitted (05-DEC-2002) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan | |
| | | | (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:-81-3-5285-1111(ex.2120), Fax:81-3-5285-1181) | |
| COMMENT | | | Lab host: TOP10 | |
| | | | Vector: pME18S-FU3 (Acc.No. AB009864) | |
| | | | R. Site1: DraIII (CACTGTGTG) | |
| | | | R. Site2: DraIII (CACCATGTG) | |
| | | | Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTCGCTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FU3. XhoI sites just outside the DraII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Custom primers used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGCG]; 3' end primer [GACCTGAGCTGAGACACA]). | |
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| Db | 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGAGAGCCCAAGAAACGCGCTGACTAC 970 |
| Db | 541 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGAGAGCCCAAGAAACGCGCTGACTAC 600 |
| Db | 971 TTGCGATTCCTCTGAGAACAGAGAACTTGGCGGTACAGTGAAGAGATTAAGAACAG 1030 |
| Db | 601 TTGCGATTCCTCTGAGAACAGAGAACTTGGCGGTACAGTGAAGAGATTAAGAACAG 660 |
| Db | 1031 GCAGTGTGAACAATGAGTGGCTGAAACAATGAGAGGACTGGAATCCCATGTTCAAGCAT 1090 |
| Db | 661 GCAGTGTGAACAATGAGTGGCTGAAACAATGAGAGGACTGGAATCCCATGTTCAAGCAT 720 |
| Db | 1091 TCAATGAGATCAGAGAGGCGCCCAAGAGGCCCATCGCTTCCCTTCAATGATCAATGTT 1150 |

| | | | | |
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| Db | 721 | TCATAGGATCAGAGGGGTGCCCAAGGGTCCCATGTGATCCCTTCATGCATCATCTT | 780 | |
| Oy | 1151 | CTGTTCAATTCATTATCCATATATCCACCTGCTCTGAGCTTTCACTCTGACTCCCTAA | 1210 | |
| Db | 781 | CT---ATTCAATTCATTCATATCATCACTGCTGCTGAGCTTTCACCTCTGACTTCTAA | 836 | |
| Oy | 1211 | CTCCATCAGACCTCTCAGCAACCATTAAGACTGCGCAGACACTGAGAAGCC | 1259 | |
| Db | 837 | CTCCATCAGACCTCTTACGTACCATTAAGACTCTGCCAGAACCGAGAAGCC | 885 | |
| RESULT 6 | | | | |
| LOCUS | COJ28741 | 606 bp | DNA | |
| DEFINITION | Sequence 14675 from Patent WO02068579. | linear | PAT 03-FEB-2004 | |
| ACCESSION | COJ28741 | | | |
| VERSION | COJ28741.1 | GI:42298386 | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | Homo sapiens (human) | | | |
| REFERENCE | Homo sapiens | | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| JOURNAL | Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W. | | | |
| FEATURES | Kits, such as nucleic acid arrays, and Myers,E.W. | | | |
| source | humaneons or transcripts, for detecting expression and other uses | | | |
| | thereof | | | |
| | Patent: WO 02068579-A 14675 06-SEP-2002; | | | |
| ORIGIN | PE Corporation (NY) (US) | | | |
| | Location/Qualifiers | | | |
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| Best Local Similarity | 99.8%; | Pred. No. 1.2e-129; | | |
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| | Mismatches | 1; | Indels | 0; |
| | Gaps | 0; | | |
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| Oy | 490 | AACCCATGAAGCTGCGCTGCATCTCTGCATGAAGAAGAAGAGAGTGAAGGCCAACG | 549 | |
| Db | 73 | AACCCATGAAGCTGCGCTGCATCTCTGCATGAAGAAGAAGAGTGAAGGCCAACG | 132 | |
| Oy | 550 | GTGTGGAATGGTTCTTACAGGCCCGCAGGCGGTAAAGATTTCTTATTTTACAGATATCG | 609 | |
| Db | 133 | GTGTGGAATGGTTCTTACAGGCCCGCAGGCGGTAAAGATTTCTTATTTTACAGATATCG | 192 | |
| Oy | 610 | AATGGCCACCAAGAGGTGAGAGCCCTTTTCAAGGGCGCTGCAAGTGAATGACAGCAAG | 669 | |
| Db | 193 | AATGGCCACCAAGAGGTGAGAGCCCTTTTCAAGGGCGCTGCAAGTGAATGACAGCAAG | 252 | |
| Oy | 670 | GACCTGCAGAGAGGTGCTCATCATCTGTGCTCAACGTCACTGAAAGCATCTGGACCTTAC | 729 | |
| Db | 253 | GACCTGCAGAGAGGTGCTCATCATCTGTGCTCAACGTCACTGAAAGCATCTGGACCTTAC | 312 | |
| Oy | 730 | ACTTGAATATGTATCCCGGAGATTGATAGTTGAGGCGCATCGGCCCTTTGTGAAGCAGAG | 789 | |
| Db | 313 | ACTTGAATATGTATCCCGGAGATTGATAGTTGAGGCGCATCGGCCCTTTGTGAAGCAGAG | 372 | |
| Oy | 790 | CGGCTGATCCCTTAAAGATCAACCGAGAGGCTGGAAGAGACTTAACTTGTGTCTCA | 849 | |
| Db | 373 | CGGCTGATCCCTTAAAGATCAACCGAGAGGCTGGAAGAGACTTAACTTGTGTCTCA | 432 | |
| Oy | 850 | GAAATCATGATGTAATCATCTTCTGTGTTTCCCTCAACCTGTGGCTGTCATGGAATGATA | 909 | |
| Db | 433 | GAAATCATGATGTAATCATCTTCTGTGTTTCCCTCAACCTGTGGCTGTCATGGAATGATA | 492 | |

| | | | |
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| OY | 910 | TATGTGTAACGAAGAGTCTCAAAAGCCGAAGAGCACCACCAAGAAAACGGTCGACTAC | 969 |
| DB | 493 | TATTGCTACAGAAGAGTGCTCAAAGGCCAAGAGCGACCCCAAGAAAACGGTCGACTAC | 552 |
| OY | 970 | CTTGCCATCCCATCTGAGAACCAAGAGACTCTGCGGTACCACTGAGAGAAATAG | 1023 |
| DB | 553 | CTTCGCATCCCATCTGAGAACCAAGAGAACTCTGCGGTACCACTGAGAGAAATAG | 606 |
| RESULT 7 | | | |
| LOCUS | BC053919 | | |
| DEFINITION | BC053919 | 4169 bp mRNA linear ROD 08-Oct-2003 | |
| ACCESSION | BC053919 | Mus musculus sodium channel, voltage-gated, type III, beta, mRNA | |
| VERSION | BC053919.1 | (cDNA clone MGC:56857 IMAGE:5308278), complete cds. | |
| KEYWORDS | MGCL | | |
| SOURCE | | | |
| ORGANISM | | Mus musculus (house mouse) | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| AUTHORS | | Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. | |
| | | 1 (bases 1 to 4169) | |
| | | Klaunig,R.L., Fellings,E.A., Grouse,L.H., Derge,J.G., | |
| | | Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., | |
| | | Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F., | |
| | | Stapleton,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., | |
| | | Scietz,T.E., Brownstein,M.J., Usdin,T.B., Tohyuki,S., | |
| | | Carrinchi,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., | |
| | | Abrahamson,R.D., Mullaly,S.J., Bosak,S.A., McGowan,P.J., | |
| | | McMernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., | |
| | | Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,S.W., | |
| | | Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., | |
| | | Raney,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., | |
| | | Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., | |
| | | Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., | |
| | | Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schwartz,J., Myers,R.M., | |
| | | Burkefield,Y.S., Krzywinski,M.I., Skalski,U., Smalls,D.E., | |
| | | Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A. | |
| | | Generation and initial analysis of more than 15,000 full-length | |
| | | human and mouse cDNA sequences | |
| JOURNAL | | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | |
| MEDLINE | | 22388257 | |
| PUBMED | | 12477932 | |
| REFERENCE | | 2 (bases 1 to 4169) | |
| AUTHORS | | Strausberg,R. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (16-JUN-2003) National Institutes of Health, Mammalian | |
| | | Gene Collection (MGC), Cancer Genomics Office, National Cancer | |
| | | Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, | |
| | | USA | |
| REMARK | | NIH-MGC Project URL: http://mgc.nci.nih.gov | |
| COMMENT | | Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: Susan L. Sullivan, Phd. cDNA Library Preparation: ReGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org Contact: amadan@systembiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting | |

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Series: IRAK Project: 105 Row: d Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943798.

Location/Qualifiers
1..4169
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Best Local Similarity 86.7%; Pred. No. 1,1e-125;
Matches 658; Conservative 0; Mismatches 97; Indels 4; Gaps 2;

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QY 386 TCAATGATGTTCCCTCCGCTTCTCTGTGCTTATCTAGGTCAGTCTGCTCC 445
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QY 446 CTGTGTGTGGAAGTCCCTCGAGACGAGGCCGTGCAAGGCAACCCCATGAAGCTGC 505
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QY 506 GCTGCACTTCTGCAAGAGAGAGAGTGAAGCCACCAAGGTGTGGAATGTTCT 565
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QY 686 CCATCACTGTGCTCAAGCTACTGAAAGCACTTGCCCTTCACTGCAATGTGTCC 745
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QY 746 GGAAGTTTGAAGTGAAGCGCATCGGCTTTGGAAGAGAGCGCGCTATCCCCCTAA 805
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QY 806 GAGTCAACGAGAGGCTGAGAGAGACTTCACTGTGTGTCTGGAATCATGATGACA 865
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RESULT 8
AX048005 2632 bp DNA linear PAT 15-DEC-2000
LOCUS Sequence 22 from Patent WO0069912.
DEFINITION AX048005
ACCESSION AX048005.1 GI:11876883
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 Curtis,R.A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 22 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
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Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATGTTTCCCTGAGCTCTCTGCTTATCTACGAG 430
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QY 491 ACCCATGAAGCTGCGCTGATCTCTGCAATGAAGAGAGAGTGAAGGCCACCAAG 550
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QY 851 AATCATGATGATACCTCTTCTGCTCTTCCCTCACCCTGTGCTGCTCATCGATGATAT 910
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RESULT 9

AF378093 3107 bp mRNA linear ROD 11-SEP-2002
LOCUS Rattus norvegicus sodium channel beta 3 subunit (SCN3B) mRNA,
complete cds.

AF378093
ACCESSION AF378093.1 GI:14165175

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

gene

CDS

ORIGIN

ORIGIN

Query Match 44.4%; Score 559.6; DB 10; Length 3107;
Best Local Similarity 84.4%; Pred. No. 7.3e-122;
Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATCCCTGCTTCAATAGATTGTTCCCTGAGCTTCTCTGCTGCTTATCTA 430
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QY 431 TCAAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
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DB 192 ATCCCATGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
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RESULT 10

AX047984

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

AX047984 3108 bp DNA linear PAT 15-DEC-2000
LOCUS Sequence 1 from Patent WO0069912.
DEFINITION AX047984
ACCESSION AX047984.1 GI:11876881
VERSION
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Rattus sp.
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
JOURNAL Rattus.
FEATURES
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Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 1 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Query Match 44.1%; Score 556.4; DB 10; Length 3910;
Best Local Similarity 84.1%; Pred. No. 4,2e-121;
Matches 653; Conservative 0; Mismatches 116; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCATATAGATTGTTCCCTGCTTCTCTGCTTATCTAATGCG 430
DB 373 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTACTAGCG 432
QY 431 TCAAGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
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QY 491 ACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
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RESULT 12
AKI73115
LOCUS AKI73115 4025 bp mRNA linear ROD 28-JUL-2004

DEFINITION Mus musculus mRNA for mKIAA1158 protein.
ACCESSION AKI73115
VERSION AKI73115.1 GI:50510814
KEYWORDS PII_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Hiraoka, S., Saga, Y., Setno, S., Nishimura, M., Kaino, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H. Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries of cDNA Res. 11, 205-218 (2004)

TITLE

JOURNAL DNA Res. 11, 205-218 (2004)

AUTHORS

Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.

JOURNAL

Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7

COMMENT

The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.

FEATURES

Location/Qualifiers
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/clone="mfj07349"
/note="vector:modified pBC SK+"

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CDS

<131..937
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/note="CDS is predicted by in silico analysis. Start codon is not identified."

/evidence="not experimental"
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LVNTLNDSCGYTCNVSRSEFEFAHPPVKTTRLIPLRYTEAEDFTSYSEI
NMVILVLTLMFLTEMLCYRKVSKAEBAQENASDYLAIPENKENSVPVEE"

ORIGIN

Query Match 43.1%; Score 543.2; DB 10; Length 4025;
Best Local Similarity 87.7%; Pred. No. 5.7e-118;
Matches 593; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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QY 409 TCTCTGCTTATATCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
DB 323 TCTCTGCTTATATCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 382
QY 469 GAGAGAGGCGCGTGCAGAGGCAACCCATGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTG 528
DB 363 GAGAGAGGCGCGTGCAGAGGCAACCCATGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTG 442
QY 529 GAGAGAGTGAAGGCAACCGTGTGAATGTTCTACAGGCGCCGAGAGGCGGTAAAGAT 588
DB 443 GAGAGAGTGAAGGCAACCGTGTGAATGTTCTACAGGCGCCGAGAGGCGGTAAAGAT 502

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QY 589 TTCCCTATTACAGATTCGGAATGGCCACGAGAGGTGAGAGAGCCCTTTCAGAGGCGC 648
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D 563 CTCAGAGGAGATGGAGCAAGAGCTTCAGAGAGCTTCATCTGCTTCATCTCAATGTCACT 622
QY 709 CTGAAGAGCTCTGGCCCTTCACCTGCAATGTGCCCCGAGAGTTGAGTTGAGGCCGAT 768
D 623 CTGAATGACTCTGGCCCTTCACCTGCAATGTGCCCCGAGAGTTGAGTTGAGGCCACAC 682
QY 769 CGGCCCCCTTGTGAAGAGCAGCGGCTGATCCCCCTTAAGATCAGCAGAGAGCTGAGAG 828
D 683 CGGCCCCCTTGTGAAGAGCAGCAGCTAATACCTTGGAGTCTCACTGAAGAGCGGAGAA 742
QY 829 GACTTCACCTCTGTGTCTCAGAAATCATGATGATCATCTTCTGTCTTCTTCACCCCTG 888
D 743 GACTTCACCTCTGGGCTCTGGAATCATGATGATCATCTTCTGTCTTCTTCACCCCTG 802
QY 889 TGCTGTCTCATCAGATGATATATTTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCC 948
D 803 TGCTGTCTCATCAGATGATATATTTGCTACAGAAAGTCTCTTAAGGCGGAGAGGCGCT 862
QY 949 CAGAAAAACGCTCTGACTGACTGCTGATCCATCCATCTGAGAACAGAGAACTGCGGTA 1008
D 863 CAGAAAAACGCTCTGACTGACTGCTGATCCATCCATCTGAGAACAGAGAACTGCTGTA 922
QY 1009 CCAAGTGGAGAGATAGA 1024
D 923 CCCGTGAGAGATAAA 938

RESULT 13
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LOCUS Mus musculus sodium channel, voltage-gated, type III, beta, mRNA
DEFINITION (cdna clone MGC:64710 IMAGE:5702879), complete cds.
ACCESSION BC058636
VERSION BC058636.1 GI:35193132
KEYWORDS Mus musculus (house mouse)
SOURCE MGC.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 4176)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Cassavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shchepetov, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.B.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED 22388257
12477932
REFERENCE 2 (bases 1 to 4176)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2003) National Institutes of Health, Mammalian

```

REMARK COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA.

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINN)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.uiowa.edu>

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu

Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>

Series: Plate: Row: Column: 0

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943798.

Location/Qualifiers

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/tissue_type="Brain, enriched mouse brain 12.5dpc"

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/note="Vector: pYX-ASC"

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/db_xref="MGI:1918882"

412. 1059

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547. 777

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gene

CDS

misc_feature

ORIGIN

Query Match 43.0%; Score 542.6; DB 10; Length 4176;

Best Local Similarity 88.2%; Pred. No. 7.9e-118;

Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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D 392 GAAGCCGCTTACAGAGAAATATGCTGCTTCAACAGATTGCTCCCTAGCTTCTAG 451

QY 416 TGCTTATCTACTGGTCAAGTGTGCTGCTCCCTGTGTGTGAAGTGGCTCGAGACG 475

D 452 TGCTTATCTACTGGTCAAGTGTGCTGCTCCCTGTGTGTGAAGTGGCTCGAGACG 511

QY 476 AGCCGCTGAGGCAACCCCATGAGCTGCTGCTTCATGAGAGAGAGAGG 535

D 512 AAGCCGCTGAGGCAATTCATGAGCTGATGATGATGATGATGATGAGAGAGAGG 571

QY 536 TGGAGCCACCAACGCTGCTGGAATGTTCTACAGCCCGGAGCGGTAAAGATTTCCTTA 595
| | | | |
DB 572 TGGAGCCACCAACGCTGCTGGAATGTTCTACAGCCCGGAGCGGTAAAGATTTCCTTA 631
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QY 536 TTTACGATGATGGAATGCGCCACCGAGGCTGGAAGACCCCTTTCAAGGGGCGCTGCACT 655
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DB 632 TATATGAGATGATGGAATGCGCCACCGAGGCTGGAAGACCCCTTTCAAGGGTCTGCACT 691
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QY 656 GGAATGCGAGCAAGAGACCTGCGAGAGCTGCTCATGCTGCTCAACGTCATCTGAAAG 715
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DB 652 GGAATGCGAGCAAGAGACCTGCGAGAGCTGCTCATGCTGCTCAACGTCATCTGAAAG 751
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QY 716 ACTCTGCGCTTACACCTGCAATGCTGCCGAGTTTGAAGGCGCATCGCCCT 775
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QY 776 TTTGTGAAGACGAGCGGCTGATCCCTTAAAGTCAACGAGAGGCTGGAAGAGACTTCA 835
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DB 812 TTTGTGAAGACGAGCGGCTGATCCCTTAAAGTCAACGAGAGGCGGAGAGACTTCA 871
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QY 836 CCTCTGCTGCTCAGAAATCATGATGATACATCTTCTGCTTCTCAACCTGCTGCTG 895
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DB 872 CCTCTGCTGCTCAGAAATCATGATGATACATCTTCTGCTTCTCAACCTGCTGCTG 931
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QY 896 TCATCGAGATGATATATGCTCTACAGAAAGTCTCAAAAGCCGAGAGCGCCCAAGAA 955
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QY 956 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
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QY 1016 AGGAATAGA 1024
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DB 1052 AGGAATAAA 1060
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RESULT 14
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DEFINITION Mus musculus brain and heart sodium channel beta 3 subunit mRNA,
complete cds.
ACCESSION AY049036
VERSION AY049036.1 GI:15822811
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 670)
AUTHORS Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
TITLE Mouse brain and heart beta 3 sodium channel cDNA
JOURNAL Unpublished
2 (bases 1 to 670)
REFERENCE 2 (bases 1 to 670)
AUTHORS Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2001) Pharmacology, University of Michigan, 1301
MSRB III, Box 0632, Ann Arbor, MI 48109-0632, USA
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ORIGIN

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Best Local Similarity 89.3%; Pred. No. 2.4e-117;
Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY 431 TCAAGTCTGCTTCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
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DB 73 TCAGAGTCTGCTTCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
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QY 491 ACCCATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
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DB 133 ATTCATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
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DB 193 TAGTGAAGTGTCTACAGGCGCGGCTAAAGATTCTTATTTACAGATTCGGA 252
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QY 611 ATGCGCACAGAGAGTGGAGAGCCCTTTCAGAGGCGCTGCTGCTGCTGCTGCTG 670
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DB 253 ATGCGCACAGAGAGTGGAGAGCCCTTTCAGAGGCGCTGCTGCTGCTGCTGCTG 312
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DB 313 ACCTGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
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QY 731 CCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790
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DB 373 CATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
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QY 791 GCGTATCCCTTAAGTCAACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
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DB 433 GACTAATACCTTGGAGTCACTGAGAGGCGGAGAGAGCTTCACTCCGAGTCTG 492
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QY 851 AATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
| | | | |
DB 433 AATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
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QY 911 ATGCTACAGAAAGTCTCAAAAGCCGAGAGAGCGCCAGAGAAACGCTTGTACTAC 970
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DB 553 ATGCTACAGAAAGTCTCAAAAGCCGAGAGAGCGCCAGAGAAACGCTTGTACTAC 612
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QY 971 TTGCAATCCCATCTGAGAGCAAGAGAACTCTGCGCTACCGATGAGAGATA 1022
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LOCUS AR359849
DEFINITION Sequence 3 from patent US 6593565.
ACCESSION AR359849
VERSION AR359849.1 GI:33766659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Heslin, P. and Lynam, N.R.
TITLE Vehicle interior rearview mirror assembly including an
accessory-containing housing
JOURNAL Patent: US 6593565-A 3 15-JUL-2003;
FEATURES location/Qualifiers
source 1..2220
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ORIGIN
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Best Local Similarity 89.3%; Pred. No. 3.3e-117;
Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY 851 AAATCATGATGTATCATCTCTTCTGCTTCTCTCACTGCTGCTGCTCATGAGTGTAT 910
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Db 838 AAATCATGATGTATCATCTCTGCTTCTCTCACTGCTGCTGCTCATGAGTGTAT 897
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QY 911 ATTGCTACAGAAAGTCTCAAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
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Db 898 ATTGCTACAGAAAGTCTCTTAAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
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Db 958 TTGCTATCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 1009
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Search completed: April 1, 2005, 20:37:25
Job time : 5670 secs

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CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostate
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1B protein encoding cDNA.

SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

| Query Match | Score | DB | Length |
|-------------|-------|----|--------|
| 100.0% | 1261 | 10 | 1261 |

Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| Oy | 61 | AAGCTGAGATTCCGGGGGTGGGGCGGGAGAGCGACTGCTCCGTGGTGTGAGACGCGCGAGAGA | 120 |
| Db | 61 | AAGCTGAGATTCCGGGGGTGGGGCGGGAGAGCGACTGCTCCGTGGTGTGAGACGCGCGAGAGA | 120 |
| Oy | 121 | GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAATCGGGAGAGTCCAGTGGGGTCCGTTAG | 180 |
| Db | 121 | GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAATCGGGAGAGTCCAGTGGGGTCCGTTAG | 180 |
| Oy | 181 | GAGCCAAAGCCCCCAACCCGGGCTCCAAAAGCTCCAGGGCTTCGCCAGGCAACCGGTCTCG | 240 |
| Db | 181 | GAGCCAAAGCCCCCAACCCGGGCTCCAAAAGCTCCAGGGCTTCGCCAGGCAACCGGTCTCG | 240 |
| Oy | 241 | GCCCTTCTTGGGTAGAAAGTCCGCCCTTGGGGGCAATTGCTCCAAAAGGGTTTCTCG | 300 |
| Db | 241 | GCCCTTCTTGGGTAGAAAGTCCGCCCTTGGGGGCAATTGCTCCAAAAGGGTTTCTCG | 300 |
| Oy | 301 | AAAGAAATGAGAGGGCGCAGTCCCTTGAACCGAGGGGAATCTCTGTGTAGACTTTGGAAGC | 360 |
| Db | 301 | AAAGAAATGAGAGGGCGCAGTCCCTTGAACCGAGGGGAATCTCTGTGTAGACTTTGGAAGC | 360 |
| Oy | 361 | CGCCAGCCCCAGAAAGATGCTGCTCTCAATAGATTGTTCCCTGGCTTCTCGTGCTT | 420 |
| Db | 361 | CGCCAGCCCCAGAAAGATGCTGCTCTCAATAGATTGTTCCCTGGCTTCTCGTGCTT | 420 |
| Oy | 421 | ATTACTGGGTCAAGTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGAGAGCGAGGCC | 480 |
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| Db | 481 | GTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTCATGAAGAGAGAGAGGTGAG | 540 |
| Oy | 541 | GCCACCAAGTGTGGAATGTTCTACAGGCCCCGAGGGCGGTAAAGATTTCTTAATTAC | 600 |
| Db | 541 | GCCACCAAGTGTGGAATGTTCTACAGGCCCCGAGGGCGGTAAAGATTTCTTAATTAC | 600 |
| Oy | 601 | GAGTATCGGAATGGCACCACGAGAGGTGAGAACCCCTTTCAGAGGGCGCTGTGAGTGAAT | 660 |
| Db | 601 | GAGTATCGGAATGGCACCACGAGAGGTGAGAACCCCTTTCAGAGGGCGCTGTGAGTGAAT | 660 |
| Oy | 661 | GGAGACAGAGACTTGCAGAGCGTGTCCATCTACGTGCTCAACGTCACTTGAAACGACT | 720 |
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| Oy | 721 | GAGCTTACACTGCATATGTGTCCCGGAGTTTGAATTGAGGCGCATCGCCCTTTGTG | 780 |
| Db | 721 | GAGCTTACACTGCATATGTGTCCCGGAGTTTGAATTGAGGCGCATCGCCCTTTGTG | 780 |
| Oy | 781 | AAGACGACGGAGTGATCCCTTAAGATCAACGAGAGGCTGAGAGAGATTCACTCTT | 840 |

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| Qy | 841 | GTGGCTTCAGAAATCATGATGTAGATCCCTTCTGCTCTTCCACCTGTGGCTCTCATC | 900 |
| Db | 841 | GTGGCTTCAGAAATCATGATGTAGATCCCTTCTGCTCTTCCACCTGTGGCTCTCATC | 900 |
| Qy | 901 | GAGATGATATATTGGTCTACAGAAAGGCTCAAAGCCGAGAGGCGCCAAAGAAACGCC | 960 |
| Db | 901 | GAGATGATATATTGGTCTACAGAAAGGCTCAAAGCCGAGAGGCGCCAAAGAAACGCC | 960 |
| Qy | 961 | TCTGACTACCTGGCATCCCATCTGAGAACAGAGGAACCTTGCGGTACCATGAGGAA | 1020 |
| Db | 961 | TCTGACTACCTGGCATCCCATCTGAGAACAGAGGAACCTTGCGGTACCATGAGGAA | 1020 |
| Qy | 1021 | TAGAACAGAGCAGTGTGACATGAGTGGCCCTGGAACCTGAGGAGTGCATCCCATG | 1080 |
| Db | 1021 | TAGAACAGAGCAGTGTGACATGAGTGGCCCTGGAACCTGAGGAGTGCATCCCATG | 1080 |
| Qy | 1081 | TTACAGCAATGTCATGATGCGATAGAGGGCGCCCAAGGGCCCATTCGCTTCCATATC | 1140 |
| Db | 1081 | TTACAGCAATGTCATGATGCGATAGAGGGCGCCCAAGGGCCCATTCGCTTCCATATC | 1140 |
| Qy | 1141 | ATCCATGTTCTGTTTCATTCATTCATCATCCACCTGCGCTCTGAGCTTTACCTCT | 1200 |
| Db | 1141 | ATCCATGTTCTGTTTCATTCATTCATCATCCACCTGCGCTCTGAGCTTTACCTCT | 1200 |
| Qy | 1201 | GACTCCCTAATCTCATCAGACCTCTAGCAGCAGCATTAAGCTCTGCGAGAACTGAGAGCCG | 1260 |
| Db | 1201 | GACTCCCTAATCTCATCAGACCTCTAGCAGCAGCATTAAGCTCTGCGAGAACTGAGAGCCG | 1260 |
| Qy | 1261 | G 1261 | |
| Db | 1261 | G 1261 | |
| RESULT 3 | | | |
| ID | ADB78651 | standard; cDNA; 1261 BP. | |
| AC | ADB78651; | | |
| DT | 04-DEC-2003 | (first entry) | |
| DE | Human ion channel subunit cDNA mutant SCN1A _r exon 1 SEQ ID NO:22. | | |
| KW | ss; gene; mutant; ion channel; ion channel subunit; ICS; nontropic; | | |
| KW | neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine; | | |
| KW | antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic; | | |
| KW | neurotropic; antidiabetic; ophthalmological; epilepsy; | | |
| KW | ion channel dysfunction; human. | | |
| OS | Synthetic. | | |
| OS | Homo sapiens. | | |
| PN | WO2003008574-A1. | | |
| PD | 30-JAN-2003. | | |
| PF | 08-JUL-2002; 2002WO-AU000910. | | |
| PR | 18-JUL-2001; 2001AU-00006452. | | |
| PR | 05-MAR-2002; 2002AU-00000910. | | |
| PR | 13-MAY-2002; 2002AU-00002292. | | |
| PA | (BION-) BIONOMICS LTD. | | |
| PA | (WALL/) WALLACE R W. | | |
| PI | Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SB; | | |
| PI | Berkovic SF, Scheffer IE; | | |
| DR | WPI; 2003-239332/23. | | |

Identifying predisposition to an ion channel dysfunction, such as periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease, schizophrenia, anxiety and depression, by detecting encoding-gene mutation events.

Claim 6, SEQ ID NO 22; 106bp; English.

The invention relates to a novel method for identifying a subject predisposed to a disorder associated with ion channel dysfunction. The method comprises ascertaining if at least one of the genes encoding ion channel subunits (ICS) has undergone a mutation event so that a cDNA derived from the subject has any of 134 nucleotide sequences. The method of the invention has nootropic, neuroprotective, inotropic, antipyretic, antiarrhythmic, antitumor, antidepressant, antiparkinsonian, antiepileptic, tranquilizer, analgesic, nephrotoxic, antidiabetic, and ophthalmological activity. A polynucleotide of the invention acts as an ion channel agonist, or ion channel antagonist. The methods, isolated nucleic acids, polypeptides, antibody, selective agonist, antagonist or modulator of an ion channel, cells and genetically modified non-human animal, are useful for the diagnosis and treatment of epilepsy and/or a disorder associated with ion channel dysfunction, such as hyper- or hypokalemic periodic paralysis, myotonia, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinulinemic hypoglycaemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour blindness. The present sequence represents a mutant cDNA of the invention. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Query Match 99.9%; Score 1259.4; DB 10; Length 1261;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGCGCAACGAGGAGGCGGCGAGTGG 60
DB 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGCGCAACGAGGAGGCGGCGAGTGG 60
QY 61 AAGCTGAGTTCCGGGGTGGGCGGAGGCGACTGCTCGTGTGTGAGCGCGCGAGAG 120
DB 61 AAGCTGAGTTCCGGGGTGGGCGGAGGCGACTGCTCGTGTGTGAGCGCGCGAGAG 120
QY 121 GCGGGCGCGAGCGGCTGATCGGCTTCCTCGAATGCGGAGGTCGATGCGGCTT 180
DB 121 GCGGGCGCGAGCGGCTGATCGGCTTCCTCGAATGCGGAGGTCGATGCGGCTT 180
QY 181 GGGCCCAAGCCCGCCCGGCTCCAAAGCTCCGAGGGGCTCCGAGGAGCGGGTCTG 240
DB 181 GGGCCCAAGCCCGCCCGGCTCCAAAGCTCCGAGGGGCTCCGAGGAGCGGGTCTG 240
QY 241 GGCCTTCCTTCGATGAGAAAGTGCCTTCGAGGAGGTCGTCCTCCAAAGGGTTCT 300
DB 241 GGCCTTCCTTCGATGAGAAAGTGCCTTCGAGGAGGTCGTCCTCCAAAGGGTTCT 300
QY 301 AAAAGATCTGAGAGGGCGGAGTCTTTGACCGAGGGAATCTCTGTGTAGCCTTGA 360
DB 301 AAAAGATCTGAGAGGGCGGAGTCTTTGACCGAGGGAATCTCTGTGTAGCCTTGA 360
QY 361 GCGCCAGCCCCAGAAATGCTGCTTCAATAGATTGTTCCCTGCTTCTCGTCTT 420
DB 361 GCGCCAGCCCCAGAAATGCTGCTTCAATAGATTGTTCCCTGCTTCTCGTCTT 420
QY 421 ATCTACTGGGTCAAGTCTGCTTCCCTGTGTGTGTGGAAGTCCCTCGGAGCGAG 480
DB 421 ATCTACTGGGTCAAGTCTGCTTCCCTGTGTGTGTGGAAGTCCCTCGGAGCGAG 480
QY 481 GTGCAAGGCAACCCCATGAAAGCTGCGCTGCAATCTCTGATGAAGAGAGAGGTGAG 540
DB 481 GTGCAAGGCAACCCCATGAAAGCTGCGCTGCAATCTCTGATGAAGAGAGAGGTGAG 540
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DB 481 GTGCAAGGCAACCCCATGAAAGCTGCGCTGCAATCTCTGATGAAGAGAGAGGTGAG 540
QY 541 GCCACCAAGTGTGTGGAATGTTCTACAGGCCCGAGGCGGTAAAGATTCTTATTAC 600
DB 541 GCCACCAAGTGTGTGGAATGTTCTACAGGCCCGAGGCGGTAAAGATTCTTATTAC 600
QY 601 GAGTATCGGAATGCGCACAGAGGTGAGAGCCCTTTCAAGGGGCGCTTCAGATG 660
DB 601 GAGTATCGGAATGCGCACAGAGGTGAGAGCCCTTTCAAGGGGCGCTTCAGATG 660
QY 661 GCGCAGCAAGACCTTCAGAGAGTGTGCTTCACTGTGCTCAACGTCACCTTGA 720
DB 661 GCGCAGCAAGACCTTCAGAGAGTGTGCTTCACTGTGCTCAACGTCACCTTGA 720
QY 721 GAGCTCTACCTGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCTTGT 780
DB 721 GAGCTCTACCTGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCTTGT 780
QY 781 AAGACGAGCGGCTGATATCCCTTAAGATCAACGAGAGGCTGAGAGACTTCACT 840
DB 781 AAGACGAGCGGCTGATATCCCTTAAGATCAACGAGAGGCTGAGAGACTTCACT 840
QY 841 GTGCTCTAGAAATATATATATATATATCTTCTGTGCTTCTTCACTGTGCTG 900
DB 841 GTGCTCTAGAAATATATATATATATATCTTCTGTGCTTCTTCACTGTGCTG 900
QY 901 GAGATGATATATATGCTACAGAAAGGCTCAAAAGCCGGAAGAGGAGCCCAAG 960
DB 901 GAGATGATATATATGCTACAGAAAGGCTCAAAAGCCGGAAGAGGAGCCCAAG 960
QY 961 TCTGATCACTTGCCTTCCATCCATCTTGAGAACAGAGAACTGTGCGGTACA 1020
DB 961 TCTGATCACTTGCCTTCCATCCATCTTGAGAACAGAGAACTGTGCGGTACA 1020
QY 1021 TAGAACAGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 TAGAACAGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 TTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 TTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 ATCCATGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTC 1200
DB 1141 ATCCATGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTC 1200
QY 1201 GACTCCCTTAATCTCAATGACCTCTTACGACCACTTAAGCTCTGCGAAGTGA 1260
DB 1201 GACTCCCTTAATCTCAATGACCTCTTACGACCACTTAAGCTCTGCGAAGTGA 1260
QY 1261 G 1261
DB 1261 G 1261
```

RESULT 4
ID ABA93727 standard; cDNA: 4052 BP.

ABA93727;
30-APR-2002 (first entry)

Human signal transduction cDNA clone amy2_2f18.

Human; foetal brain; foetal kidney; melanoma; testis; amygdala;

gene therapy; ss.

Homo sapiens.

WO200198454-A2.

27-DEC-2001.

XX 25-APR-2001; 2001MO-IB002050.
 XX 25-APR-2000; 2000US-0199380P.
 PR (GEHU-) GERMAN HUMAN GENOME PROJECT.
 PA Wiemann S;
 PI WPI: 2002-055860/07.
 DR P-PSDB; ABB05689.
 XX Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy.
 XX Claim 1; Page 174-175; 611pp; English.
 PS
 XX The present invention describes assemblies and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC fetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures
 CC
 XX Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
 SQ
 Query Match: 99.3%; Score 1252.2; DB 6; Length 4052;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 971 CACCACGGTGTGAATGTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTACGA 1030
 Qy 603 GTATCGGAATGCGCACCAGAGAGTGGAGGCCCTTACAGGGCGCTGAGTGAATGG 662
 Db 1031 GTATCGGAATGCGCACCAGAGAGTGGAGGCCCTTACAGGGCGCTGAGTGAATGG 1090
 Qy 663 CACCAAGAGCCTGACGAGAGTGTCCATCACTGTGCTCAACGACTCTGAACACTCTGG 722
 Db 1091 CACCAAGAGCCTGACGAGAGTGTCCATCACTGTGCTCAACGACTCTGAACACTCTGG 1150
 Qy 723 CCTCTACCTGCAATGTGTCCCGGAGATTGAGTTGAGCGCATCGCCCTTTGTAA 782
 Db 1151 CCTCTACCTGCAATGTGTCCCGGAGATTGAGTTGAGCGCATCGCCCTTTGTAA 1210
 Qy 783 GACGAGCGGCTGATCCCTTAAGATCACCGAGAGGCTGAGAGAGACTTCACTCTGT 842
 Db 1211 GACGAGCGGCTGATCCCTTAAGATCACCGAGAGGCTGAGAGAGACTTCACTCTGT 1270
 Qy 843 GGTCTGGAATCATGATGATCATCTCTGTGCTTCTCCTCACCCTGTGCTCATCGA 902
 Db 1271 GGTCTGGAATCATGATGATCATCTCTGTGCTTCTCCTCACCCTGTGCTCATCGA 1330
 Qy 903 GATGATATATTTGCTACAGAAAGTCTCAAAAGCCGAAAGAGCAGCCCAAGAAACGGCTC 962
 Db 1331 GATGATATATTTGCTACAGAAAGTCTCAAAAGCCGAAAGAGCAGCCCAAGAAACGGCTC 1390
 Qy 963 TGACTACTTGTGCTATCCCATCTGAGAACCAAGAGAACTCTGCGGTACCACTGAGAGATA 1022
 Db 1391 TGACTACTTGTGCTATCCCATCTGAGAACCAAGAGAACTCTGCGGTACCACTGAGAGATA 1450
 Qy 1023 GAACAGAGAGAGTGTGATCATGAGTGGCTGAAACCTGAGAGAGTGTGATCCATGTT 1082
 Db 1451 GAACAGAGAGAGTGTGATCATGAGTGGCTGAAACCTGAGAGAGTGTGATCCATGTT 1510
 Qy 1083 CAGCAATGTCAATGAGCATCAGAGAGGCGCCCAAGGGCCCATCGCTTCCCTTCATGAT 1142
 Db 1511 CAGCAATGTCAATGAGCATCAGAGAGGCGCCCAAGGGCCCATCGCTTCCCTTCATGAT 1570
 Qy 1143 CCAATTGTTCTGTTCAATTCATTCATATCATATCCACTGCTTGAAGCTTCACTCTGA 1202
 Db 1571 CCAATTGTTCTGTTCAATTCATTCATATCCACTGCTTGAAGCTTCACTCTGA 1630
 Qy 1203 CTCCTTAACCTCATCAGACCTCTACGCAACATTAAGCTCTGCGCAGAACTGAGAAGCC 1259
 Db 1631 CTCCTTAACCTCATCAGACCTCTACGCAACATTAAGCTCTGCGCAGAACTGAGAAGCC 1687

RESULT 5
 AAF84146
 ID AAF84146 standard; cDNA; 1510 BP.
 AC AAF84146;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human novel sodium channel beta1-like subunit encoding cDNA.
 XX
 KW Sodium channel; sensory neurone specific channel; beta1-like subunit;
 KM SNS; therapeutic; pain; analgesic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..860
 FT /*tag= a
 FT /product= "sodium channel beta1-like subunit"
 PN MO200144293-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 14-DEC-2000; 2000MO-GB004802.
 XX

| | | |
|-----------------------|--|-----------------|
| XX | 17-DEC-1999; | 99GB--00029970. |
| PA | (GLAX) GLAXO GROUP LTD. | |
| PI | Plumpton M., Powell AJ, Sanseau P; | |
| DR | WPI; 2001-398129/42. | |
| DR | P-PSDB; AAB85206. | |
| PT | Novel sub-unit for voltage-gated sodium channel proteins for producing agents useful for treating pain. | |
| PS | Claim 4; Page 29-30; 31pp; English. | |
| CC | The invention provides a novel beta1-like sub-unit for voltage-gated sodium ion channel polypeptide, specifically a sensory neurone specific channel (SNS) subunit. The novel beta1-like subunit is useful for producing a therapeutic agent which is useful treating pain in a patient. The subunit can be expressed by standard recombinant methodology. The present sequence represents a human novel sodium channel beta1-like subunit encoding cDNA | |
| SQ | Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other; | |
| Query Match | 72.1%; Score 909.4; DB 4; Length 1510; | |
| Best Local Similarity | 99.9%; Pred. No. 3,4e-234; | |
| Matches | 910; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | |
| OY | AGCCTTGAACGCCGCGACGCCAAGAATGCCTGCTCAATAGATTGTTCCTGGACT | 408 |
| Db | 186 AGCCTTGAAAGCCGCGACGCCAAGAATGCCTGCTCAATAGATTGTTCCTGGACT | 245 |
| OY | TCTCTCGTCTTAATCTACTGAGTCAAGTCTGCTTCCGTGTGTGTGAAGTGCCTCG | 468 |
| Db | 246 TCTCTCGTCTTAATCTACTGAGTCAAGTCTGCTTCCGTGTGTGTGAAGTGCCTCG | 305 |
| OY | GAGACGAGAGCGCGTGCAGGAGCAACCCCATGMAAGCTGCCTGTATCTCTGATGAAGA | 528 |
| Db | 306 GAGAGGAGGCGCGTGCAGGAGCAACCCCATGMAAGCTGCCTGTATCTCTGATGAAGA | 365 |
| OY | GAGAGAGGAGAGCGCACCAACCGGTGTGGAATGGTTCTACAGAGCCCGAGGCGGTAAAGAT | 588 |
| Db | 366 GAGAGAGGAGAGCGCACCAACCGGTGTGGAATGGTTCTACAGAGCCCGAGGCGGTAAAGAT | 425 |
| OY | TYTCTTAATTTACAGATATCGAATGGACCACAGAGAGTGAAGAGCCCTTTCAAGGAGCGC | 648 |
| Db | 426 TYTCTTAATTTACAGATATCGAATGGACCACAGAGAGTGAAGAGCCCTTTCAAGGAGCGC | 485 |
| OY | CTGCAGTGAATGATGACAGAACGACTGTCAGAGACGTGTCTATCATCTGTGCTCAAGTCACT | 708 |
| Db | 486 CTGCAGTGAATGATGACAGAACGACTGTCAGAGACGTGTCTATCATCTGTGCTCAAGTCACT | 545 |
| OY | CTGAACGACTCTGGGCTCTACACCTCGAATGTGTCCGGAGATTGAGTTGAGGCGGAT | 768 |
| Db | 546 CTGAACGACTCTGGGCTCTACACCTCGAATGTGTCCGGAGATTGAGTTGAGGCGGAT | 605 |
| OY | CGGCCCCCTTGTGAACAACGACGCGGTGTATCCCCCTTAAGAGTCAACGAGAGGCTGAAG | 828 |
| Db | 606 CGGCCCCCTTGTGAACAACGACGCGGTGTATCCCCCTTAAGAGTCAACGAGAGGCTGAAG | 665 |
| OY | GACTTCACCTCTGTGTGTCTCAGAAATCATGATGTATCATCTTCTGTGTCTTCTCACTCGT | 888 |
| Db | 666 GACTTCACCTCTGTGTGTCTCAGAAATCATGATGTATCATCTTCTGTGTCTTCTCACTCGT | 725 |
| OY | TGGCTGCTCATTCGAATGATATATTGTCTACAGAAAGGTCTCAAAGCCGGAAGAGGCAACC | 948 |
| Db | 726 TGGCTGCTCATTCGAATGATATATTGTCTACAGAAAGGTCTCAAAGCCGGAAGAGGCAACC | 785 |
| OY | CAAGAAAACGCGTCTGACTACCTTGCATCCATCTGAGAACCAAGAGAACTCTCGGATA | 1008 |
| Db | 786 CAAGAAAACGCGTCTGACTACCTTGCATCCATCTGAGAACCAAGAGAACTCTCGGATA | 845 |
| OY | 1009 CCAGTGAAGAAATGAACAAGAGACAGTGTGACATGAGGTGGCTTGAAACCTTGAGGAACT | 1068 |

| | | | | |
|----------|---|--|-------------|-----|
| Db | 846 | CCAGTGGAGGAATGAAACAGGAGCAGTGTGACATAGAGGTGGCCTGAACA | CTGAGGAGACT | 905 |
| Oy | 1069 | GGACATCCCATGTTGAGCAATGTCAATGGCATCAGAGGGGGCCCCCAAGGGCCCCATCGC | | 112 |
| Db | 906 | GGACATCCCATGTTGAGCAATGTCAATGGCATCAGAGGGGGCCCCCAAGGGCCCCATCGC | | 965 |
| Oy | 1129 | TTCCCTTATGATGCATTCATTTGTTCTGTTCAATTCATTCATCAATACATCCACTGCTCTGA | | 118 |
| Db | 966 | TTCCCTTATGATGCATTCATTTGTTCTGTTCAATTCATTCATCAATCCACTGCTCTGA | | 102 |
| Oy | 1189 | GCTTTCACCTCTGACTGCTCCCTTAAGTCCATCAGACCTTAAGCAGCATTAAGACTCTGCGAGA | | 124 |
| Db | 1026 | GCTTTCACCTCTGACTGCTCCCTTAAGTCCATCAGACCTTAAGCAGCATTAAGACTCTGCGAGA | | 108 |
| Oy | 1249 | ACTGAGAAAGCC | 1259 | |
| Db | 1086 | ACTGAGAAAGCC | 1096 | |
| RESULT 6 | | | | |
| XX | AAK52345 | | | |
| ID | AAK52345 | standard; cDNA; 1045 BP. | | |
| AC | AAK52345; | | | |
| XX | | | | |
| DT | 06-NOV-2001 | (first entry) | | |
| XX | | | | |
| DE | Human polynucleotide SEQ ID NO 890. | | | |
| XX | | | | |
| KM | Human; cytokine; cell proliferation; cell differentiation; gene therapy; | | | |
| KM | vaccine; peptide therapy; stem cell growth factor; haematopoiesis; | | | |
| KM | tissue growth factor; immunomodulatory; cancer; leukaemia; | | | |
| XX | nervous system disorder; arthritis; inflammation; ss. | | | |
| OS | Homo sapiens. | | | |
| XX | | | | |
| FN | WO200157190-A2. | | | |
| PD | 09-AUG-2001. | | | |
| XX | | | | |
| PF | 05-FEB-2001; 2001WO-US004098. | | | |
| XX | | | | |
| PR | 03-FEB-2000; 2000US-00496914. | | | |
| PR | 27-APR-2000; 2000US-00560875. | | | |
| PR | 20-JUN-2000; 2000US-00598075. | | | |
| PR | 19-JUL-2000; 2000US-00620325. | | | |
| PR | 01-SEP-2000; 2000US-00654936. | | | |
| PR | 15-SEP-2000; 2000US-00663561. | | | |
| PR | 20-OCT-2000; 2000US-00693325. | | | |
| PR | 30-NOV-2000; 2000US-00728422. | | | |
| XX | | | | |
| PA | (HYSE-) HYSEQ INC. | | | |
| XX | | | | |
| PI | Tang YT, Liu C, Dirmnac RT, Asundi V, Zhou P, Xu C, Cao Y; | | | |
| PI | Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; | | | |
| PI | Xue AJ, Yang Y, Wejhrman T, Goodrich R; | | | |
| XX | | | | |
| DR | WPI: 2001-476283/51. | | | |
| XX | P-PsDB; AAM79212. | | | |
| PT | | | | |
| XX | Nucleic acids encoding polypeptides with cytokine-like activities, useful | | | |
| XX | in diagnosis and gene therapy. | | | |
| PS | Claim 1; Page 2934-2935; 6221p; English. | | | |
| XX | | | | |
| CC | The invention relates to polynucleotides (AAK51456-AAK53435) and the | | | |
| CC | encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to | | | |
| CC | cytokine, cell proliferation or cell differentiation or which may induce | | | |
| CC | production of other cytokines in other cell populations. The | | | |
| CC | polynucleotides and polypeptides are useful in gene therapy, vaccines or | | | |
| CC | peptide cell growth factor activity, haematopoiesis regulating | | | |
| CC | e.g. stem cell growth factor activity, haematopoiesis regulating | | | |


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QY 326 TGACCGAGGAATCTCTGTGTAGCTTGAAGCGCCAGCCCGAGAGATGCTGCT 385
DB 245 TCACCGAGGAATCTCTGTGTAGCTTGAAGCGCCAGCCCGAGAGATGCTGCT 304
QY 386 TCAATAGATTTTCCCTGCTGCTTCTGTGTAGCTTGAAGCGCCAGAGATGCTGCT 445
DB 305 TCAATAGATTTTCCCTGCTGCTTCTGTGTAGCTTGAAGCGCCAGAGATGCTGCT 364
QY 446 CTGTGTGTGTGAAGTGCCTCGAGACGAGAGCGCTGAGAGGCAACCCCATGAAGTGC 505
DB 365 CTGTGTGTGTGAAGTGCCTCGAGACGAGAGCGCTGAGAGGCAACCCCATGAAGTGC 424
QY 506 GCTGATCTCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
DB 425 GCTGATCTCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 566 AAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625
DB 485 AAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
QY 626 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 685
DB 545 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
QY 686 CCATCACTGTGTCAACGCTCACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745
DB 605 CCATCACTGTGTCAACGCTCACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
QY 746 GGAATTTGAAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 805
DB 665 GGAATTTGAAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
QY 806 GAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 865
DB 725 GAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 784
QY 866 TCCCTTCTGTGTCTCTCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 924
DB 785 TCCCTTCTGTGTCTCTCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 844
QY 925 GCTTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
DB 845 GCTTCAAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
QY 984 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 905 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
```

RESULT 8

ADSL1487

ADSL1487 standard; DNA; 978 BP.

ADSL1487;

16-DEC-2004 (first entry)

Human therapeutic contig DNA - SEQ ID 1724.

antiinflammatory; neuroprotective; antianaemic; cyrostatic; vulnerary;
inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

Homo sapiens.

WO2004080148-A2.

23-SEP-2004.

30-SEP-2003; 2003WO-US030720.

02-OCT-2002; 2002US-0416186P.

XX

(NUVE-) NUVELO INC.

Tang YF, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
WPI; 2004-668857/65.
P-PSDB; ADS12085.

New polynucleotide, useful in preparing a composition for diagnosing or
treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
aplastic anemia or cancer for promoting wound healing.

Example 2; SEQ ID NO 1724; 718bp; English.

The invention relates to a novel isolated polynucleotide and the encoded
polypeptide. The molecules of the invention demonstrate antiinflammatory,
neuroprotective, antianaemic, cyrostatic and vulnerary activities and may
be useful in preparing a composition for diagnosing or treating
inflammatory, haematopoietic, immune, neurodegenerative or stem cell
disorders, such as aplastic anaemia or cancer, as well as for promoting
wound healing. The molecules may also be utilised during gene therapy
procedures. The current sequence is that of a human therapeutic contig
DNA of the invention. The current sequence is not shown explicitly within
the specification but can be accessed from the WPI web-site.

Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 68.1%; Score 858.6; DB 13; Length 978;

Best Local Similarity 96.2%; Pred. No. 1.4e-220; Mismatches 34; Indels 2; Gaps 2;

Matches 901; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

86 GAGGCGACTGTCCTGT 145

5 GTGGGCGACTGTCCTGT 64

146 CCTTGAACTGAGAGAGT 205

65 CCTTGAACTGAGAGAGT 124

206 AAAGCTCCAGAGAGAGT 265

125 AAAGCTCCAGAGAGAGT 184

266 CCCCTGAGAGAGAGT 325

185 CCCCTGAGAGAGAGT 244

326 TGACCGAGAGAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 385

245 TGACCGAGAGAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 304

386 TCAATAGATTTTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 445

305 TCAATAGATTTTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 364

446 CTGTGTGTGTGAAGTGCCTCGAGACGAGAGCGCTGACAGAGCAACCCCATGAAGTGC 505

365 CTGTGTGTGTGAAGTGCCTCGAGACGAGAGCGCTGACAGAGCAACCCCATGAAGTGC 424

506 GCTGATCTCTGATGAAG 565

425 GCTGATCTCTGATGAAG 484

566 ACAGGCCGAG 625

485 ACAGGCCGAG 544

626 TGAAG 685

545 TGAAG 604

686 CCATCACTGTGTCAACGCTCACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745

605 CCATCACTGCTGTCACGTCATCTGTAGACGACTCTGACCTCTACACCTGCAATGTGTCCC 664
664
746 GGGAGTTTGAAGTTGAGGCGCATCGCCCTTTGTGAGAGAGACGCGGCTGATCCCCCTAA 805
805
665 GGGAGTTTGAAGTTGAGGCGCATCGCCCTTTGTGAGAGAGACGCGGCTGATCCCCCTAA 724
724
806 GAGTCACCGAGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATCATGATGTACA 865
865
725 GAGTCACCGAGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATCATGATGTACA 784
784
866 TCCCTTCGCTCTCCATACCTGCTGCTGCTGCTCATCGATGATATATTTG-CTACAGAAAG 924
924
785 TCCCTTCGCTCTCCATACCTGCTGCTGCTGCTCATCGATGATATATTTG-CTACAGAAAG 844
844
925 GTCCTCAAAAGCCGAG 983
983
845 GTGATCACACACGAGACGAG 904
904
984 TGAGAAACAG 1020
1020
905 TGAGAAACAG 941
941

RESULT 9
ADSI0151
ID ADSI0151 standard; DNA; 953 BP.
XX
AC ADSI0151;
XX
DT 16-DEC-2004 (first entry)
DE Human therapeutic DNA - SEQ ID 388.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytosstatic; vulnerary;
inflammatory; haemotopoiesis; immunity; neurodegenerative; stem cell;
aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX
OS Homo sapiens.
XX
PN MO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003MO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Agundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
DR P-PSDB; ADSI0835.
XX
WPI; 2004-668857/65.
XX
PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
PS Claim 1; SEQ ID NO 388; 718bp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cyostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;

Query Match 62.8%; Score 792.4; DB 13; Length 953;
Best Local Similarity 99.3%; Pred. No. 9e-203;
Matches 796; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
86 GAGGCGCATCTGCTCGGTGTGTGAGCCCGGCGAGACCGGCGGAGAGCGGCTATGCGCT 145
37 GTGGCGCATCTGCTCGGTGTGTGAGCCCGGCGAGACCGGCGGAGAGCGGCTATGCGCT 96
146 CCCTCCGAACCTGGGAGAGTCCAGTGGGGTGGCTTATGAGGCCCAAGCCCGGCTCCCA 205
97 CCCTCCGAACCTGGGAGAGTCCAGTGGGGTGGCTTATGAGGCCCAAGCCCGGCTCCCA 156
206 AAGACTCCGAGGAGCTCCCGAGGACACCGGAGCTCGGCCCTTCTCGGTGAGAAAGTGC 265
157 AAGACTCCGAGGAGCTCCCGAGGACACCGGAGCTCGGCCCTTCTCGGTGAGAAAGTGC 216
266 CCCCTGGGGGCACTTCTGCTCCCAAGGGGTTTCTCGAAAGATCTGAGAGGCGCAGTCT 325
217 CCCCTGGGGGCACTTCTGCTCCCAAGGGGTTTCTCGAAAGATCTGAGAGGCGCAGTCT 276
326 TGACCGAGGAGATCTCTGTGTGAGCCCTTGAAAGCCCGCAGAGCCCGCAGAGATGCTGCT 385
277 TGACCGAGGAGATCTCTGTGTGAGCCCTTGAAAGCCCGCAGAGCCCGCAGAGATGCTGCT 336
386 TCAATGATTGTTTCCCTGGGCTTCTGTGTGAGCCCTTGAAAGCCCGCAGAGATGCTGCT 445
337 TCAATGATTGTTTCCCTGGGCTTCTGTGTGAGCCCTTGAAAGCCCGCAGAGATGCTGCT 386
446 CTGTGTGTGTGAGAGTGCCTCGAGAGACGAGGCGGTGAGGAGCAACCCCATGAGTGC 505
397 CTGTGTGTGTGAGAGTGCCTCGAGAGACGAGGCGGTGAGGAGCAACCCCATGAGTGC 456
506 GCTGCAATCTCTGCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
457 GCTGCAATCTCTGCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
566 ACAGGCCCGAGGCGGTGAAAGATTTCTTATTAGAGATGCGAATGCGACACAGAGAG 625
517 ACAGGCCCGAGGCGGTGAAAGATTTCTTATTAGAGATGCGAATGCGACACAGAGAG 576
626 TGAGAGAGCCCTTTCAGGAGGCGCTGCACTGAGATGAGAGAGAGAGAGAGAGAGAGAG 685
577 TGAGAGAGCCCTTTCAGGAGGCGCTGCACTGAGATGAGAGAGAGAGAGAGAGAGAGAG 636
686 CCATCACTGTGCTCAACGTCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745
637 CCATCACTGTGCTCAACGTCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
746 GGGAGTTTGAAGTTGAGGCGCATCGGCCCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 805
697 GGGAGTTTGAAGTTGAGGCGCATCGGCCCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 756
806 GAGTCACCGAGAGAGGCTGAG 865
757 GAGTCACCGAGAGAGGCTGAG 816
866 TCCCTTCGCTCTCCATACCTGCTGCTGCTGCTCATCGATGATATATTTG-CTACAGAAAG 924
817 TCCCTTCGCTCTCCATACCTGCTGCTGCTGCTCATCGATGATATATTTG-CTACAGAAAG 844

RESULT 10
AAS86764
ID AAS86764 standard; cDNA; 1195 BP.
XX
AC AAS86764;
XX
DT 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #22568.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI, 2001-639362/73.
XX P-PSDB; AB622577.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostic, forensic, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 22568; 103bp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotide are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 U; 0 Other;

Query Match 44.6%; Score 561.8; DB 5; Length 1195;
Best Local Similarity 95.8%; Pred. No. 1.2e-140;
Matches 599; Conservative 0; Mismatches 22; Indels 4; Gaps 2;

QY 349 AGCCTTGAAAGCCGCGAGCCCAAGATGCTGCTTCAATAGATTGTTCCCTGAGCT 408
DB 436 AGCCTTGAAAGCCGCGAGCCCAAGATGCTGCTTCAATAGATTGTTCCCTGAGCT 495
QY 409 TCTCTGCTGCTTATCTACTGAGTGTGCTGCTTCCCTGCTGTGTGGA--GTGCCCT 466
DB 496 TCTCTGCTGCTTATCTACTGAGTGTGCTGCTTCCCTGCTGTGTGGAAGTGCCTT 555
QY 467 CGGAAGCGAGGCGCGTGA--GGGCAACCCCAAGAGCTGGCTGATCTCCGATGAA 524
DB 556 AAAAAACGGGGGCGCGAGCGGCTTAACCCCAAGAGCTGGCTGATCTCCGATGAA 615
QY 525 GAGAGAGAGGTGAGAGCCACCAAGTGTGGAATGTTCTACAGGCCCGAGGGCGGTAA 584
DB 616 GAGAGAGAGGTGAGAGCCACCAAGTGTGGAATGTTCTACAGGCCCGAGGGCGGTAA 675
QY 585 AGATTTCCTTATTATTCAGATTCGAATGGCCACAGAGGTGAGAGGCCCTTTCAAGG 644
|||||

DB 676 AGATTTCCTTATTATTCAGATTCGAATGGCCACAGAGGTGAGAGGCCCTTTCAAGG 735
QY 645 GCGCTGAGTGAATGGCAGCAAGAGCTTGACAGAGCTGTCCATCACTGTGCTCAAGCT 704
DB 736 GCGCTGAGTGAATGGCAGCAAGAGCTTGACAGAGCTGTGCTCAAGCT 795
QY 705 CACTGTGAAGCACTGTGAGCTTCTACCTGCAATGTGTCCGGAGATTGATTGAGGC 764
DB 796 CACTGTGAAGCACTGTGAGCTTCTACCTGCAATGTGTCCGGAGATTGATTGAGGC 855
QY 765 GCATCGGCCCTTTGAAAGACAGCGGCTGATCCCCCTAAGATCAACGAGAGGCTGG 824
DB 856 GCATCGGCCCTTTGAAAGACAGCGGCTGATCCCCCTAAGATCAACGAGAGGCTGG 915
QY 825 AGAGACTTCACTCTGTGTCTCAAGAAATCATATGATCATCTTGTGTTCTCTCAC 884
DB 916 AGAGACTTCACTCTGTGTCTCAAGAAATCATATGATCATCTTGTGTTCTCTCAC 975
QY 885 CCTGTGCTGCTCATCGAGATGATATTTGCTACAGAAAGGTTCAAAAGCCGAAGAGGC 944
DB 976 CTTGTGGCTGCTCATCGAGATGATATTTGCTACAGAGGTTCAAAAGCCGAAGAGGC 1035
QY 945 AGCCCAAGAAACGGGTCTGACTAC 969
DB 1036 AGCCCAAGAAACGGGTCTGACTAC 1060

RESULT 11

AAC90602
ID AAC90602 standard; DNA; 2632 BP.

AC AAC90602;
XX 13-MAR-2001 (first entry)
XX

DE Rat sodium channel beta3 protein Alrx94h5 related sequence.

XX Rat; sodium channel beta3 protein; Alrx94h5; pair; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction; ds.
XX

OS Rattus sp.

FN WO200069912-A1.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US013144.

PR 14-MAY-1999; 99US-0134198P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

DR WPI, 2001-122743/13.

XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.

PS Claim 1; Page 41-42; 145pp; English.

XX The present invention provides the protein and coding sequences of the
CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is
CC involved in the generation of pain and other sensory or perceptible nerve
CC impulses, in the establishment and endurance of mood, neurodegenerative
CC and sleep disorders, and in the control of muscle contraction, including
CC movements such as the heartbeat, digestion and vascular tone. The
CC sequences can be used in predictive medicine, screening and diagnostic
CC assays, and in pharmacogenomics

XX Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 U; 0 Other;

Query Match 44.4%; Score 559.6; DB 5; Length 2632;
 Best Local Similarity 84.4%; Pred. No. 6.5e-140;
 Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTATCTACTGCG 430
 DB 73 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTATGCTCATCTACTGCG 132
 QY 431 TCAGTGTCTGCTTCCCTGCTTGTGTGTAAGTCCCTGCGAGACGAGCCGTGAGGCA 490
 DB 133 TCAGAGTCTGCTTCCCTGCTTGTGTGTAAGTCCCTGCGAGACGAGCCGTGAGGCA 192
 QY 491 ACCCATGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
 DB 193 ATCCATGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
 QY 551 TGTGTGAATGTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTTTACAGATGGA 610
 DB 253 TGTGTGAATGTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTTTACAGATGGA 312
 QY 611 ATGGCCACCGAGAGTGTGAGAGACCCCTTTCAAGGGGCGCTGCTGCTGCTGCTGCTGCT 670
 DB 313 ATGGCCACCGAGAGTGTGAGAGACCCCTTTCAAGGGGCGCTGCTGCTGCTGCTGCTGCT 372
 QY 671 ACCTCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
 DB 373 ACCTCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
 QY 731 CTTGCAATGTGTCCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAAGCAGCG 790
 DB 433 CATGCAATGTGTCCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAAGCAGCG 492
 QY 791 GGCTGATCCCCCTTAAGTGTACCGAGAGGCTGTGAAGAGACTTCACTCTGTGTCTGAG 850
 DB 493 GACTGATACCTTTGCGAGTCACTGAAGAGCGGAGAGAGACTTCACTCTGTGTCTGAG 552
 QY 851 AAATCATGATGTACATCTTCTGCTTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910
 DB 553 AAATCATGATGTACATCTTCTGCTTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
 QY 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACGCGTCTGACTACC 970
 DB 613 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACGCGTCTGACTACC 672
 QY 971 TTGCGCATCCCATCTGAGAGACAGAGAACTCTGCGGTACCAAGTGTGAGAGAAATAGAACAGGA 1030
 DB 673 TTGCGCATCCCATCTGAGAGACAGAGAACTCTGCGGTACCAAGTGTGAGAGAAATAGAACAGGA 726
 QY 1031 GCAGTGTGATGATGAGGCTGTAACACCTGAGGAGCTGTGACATCCCATGTTTACAGCAATG 1090
 DB 727 GTGCTGTGATGATGAGGCTGTAACACCTGAGGAGCTGTGACATCCCATGTTTACAGCAATG 785
 QY 1091 TCATGTCATCAGAGAGGCGCCCAAGAGGCGCCCATGCTTCCCTTACATGATCAT 1146
 DB 786 CCAGCAATATCAGAGAGTGTGCCCAAGTGTGCCCAACATCATCTTTTCAATTCAT 841

RESULT 12
 AAC90600
 ID AAC90600 standard; cDNA; 3108 BP.
 XX AAC90600;
 AC
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE
 XX
 XX
 Rat sodium channel beta3 protein Alrx94h5 coding sequence.
 XX
 Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction; ss.
 XX
 OS Rattus sp.
 XX
 PN M0200069912-A1.

XX
 XX 23-NOV-2000.
 PD
 XX
 PF 12-MAY-2000; 2000MO-US013144.
 XX
 PR 14-MAY-1999; 99US-0134198P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Curtis RAB;
 PT
 XX
 DR WPI; 2001-122743/13.
 DR P-PSDB; AAB50243, AAB50245.
 XX
 PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.
 XX
 PS Claim 1; Fig 1; 145pp; English.

CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics

XX
 XX
 SQ Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Query Match 44.4%; Score 559.6; DB 5; Length 3108;
 Best Local Similarity 84.4%; Pred. No. 7e-140;
 Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

QY 371 AGAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTGCTTATCTACTGCG 430
 DB 73 AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTATGCTCATCTACTGCG 132
 QY 431 TCAGTGTCTGCTTCCCTGCTTGTGTGTAAGTCCCTGCGAGACGAGCCGTGAGGCA 490
 DB 133 TCAGAGTCTGCTTCCCTGCTTGTGTGTAAGTCCCTGCGAGACGAGCCGTGAGGCA 192
 QY 491 ACCCATGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
 DB 193 ATCCATGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
 QY 551 TGTGTGAATGTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTTTACAGATGGA 610
 DB 253 TGTGTGAATGTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTTTACAGATGGA 312
 QY 611 ATGGCCACCGAGAGTGTGAGAGACCCCTTTCAAGGGGCGCTGCTGCTGCTGCTGCTGCT 670
 DB 313 ATGGCCACCGAGAGTGTGAGAGACCCCTTTCAAGGGGCGCTGCTGCTGCTGCTGCTGCT 372
 QY 671 ACCTCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
 DB 373 ACCTCAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
 QY 731 CTTGCAATGTGTCCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAAGCAGCG 790
 DB 433 CATGCAATGTGTCCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAAGCAGCG 492
 QY 791 GGCTGATCCCCCTTAAGTGTACCGAGAGGCTGTGAAGAGACTTCACTCTGTGTCTGAG 850
 DB 493 GACTGATACCTTTGCGAGTCACTGAAGAGCGGAGAGAGACTTCACTCTGTGTCTGAG 552
 QY 851 AAATCATGATGTACATCTTCTGCTTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910
 DB 553 AAATCATGATGTACATCTTCTGCTTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
 QY 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACGCGTCTGACTACC 970

Db 613 ATTGCTACAGAAAGTCTCTTAAGCCGAGAGGACAGCAAGAAAATGCTGTGACTACC 672
Qy 971 TTGCCATCCCATCTGTGAGAACAGAGAACTCTGCGGTACAGTGAGAGAAATGAAACAGA 1030
Db 673 TTGCTATCCCTTCAGAGAACAGAGAACTCTGTGTACTCTGTGAGAGAAAT-AT 726
Qy 1031 GGAGTGTGACATGAGGTGGCTTGAAACCTGAGGAGCTGAGACATCCCATGTTTCAAGATG 1090
Db 727 GTGGTGTGACTGTGAGGTGATCTG-AGTGTGAGGAGCTGGATATCCCACTTCAAGTATG 785
Qy 1091 TCAATGAGCATCAGAGAGGCGCCCAAGAGGCCCTGCTTCCCTTCATCATTCAT 1146
Db 786 CCAGCAATATCAGAGAGTGCCCAAGGTGTCCCAACATCCATCTTTCTATTTCAT 841

RESULT 13

AAC67836
ID AAC67836 standard; cDNA; 2220 BP.
AC AAC67836;
XX
XX 15-FEB-2001 (first entry)
DE Rat beta3 subunit cDNA.
XX
XX Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
KM vasotrophic; cardiant; nootropic; cytostatic; dermatological;
KM gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
KM ischaemia; heart disease; Jacobsen Syndrome;
KM familial nonchromaffin paraganglioma; phenylketonuria;
KM Charcot Marie Tooth disease; ss.
XX
XX Rattus sp.
OS
XX WO20006367-A1.
PN 26-OCT-2000.
XX
XX 24-FEB-2000; 2000WO-EP001783.
PF
XX 15-APR-1999; 99US-0129473P.
PR
XX (WARN) WARNER LAMBERT CO.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Cox P, Dixon A, Jackson A, Morgan K;
PI WPI; 2000-665241/64.
DR P-PSDB; AAB36001.
XX
XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
PT stroke.
XX
XX Claim 6; Page 69-70; 88pp; English.
XX
XX The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
XX Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

Query Match 42.8%; Score 540; DB 3; Length 2220;
Best Local Similarity 89.3%; Pred. No. 1.2e-134;
Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 371 AGAAGTCCCTGCTTCATATGATTTTCCCTGCTTCTCTGCTTACTACTGG 430
Db 358 AAAAGATCCCTGCTTCAACAGATTTGCTTCCCTAGCTTCTCTAGTCTACTACTGG 417
Qy 421 TCAGTGTCTGCTTCCCTGTGTGTGTGAAGTCCCTCGAGACGAGGCCGTGACAGGCA 490
Db 418 TCAGAGTCTGCTTCCCTGTGTGTGTGAAGTCCCTCGAGACAGAACGGGTGACAGGCA 477
Qy 491 ACCCATAGCTGCGTCATCTCTGTCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550
Db 478 ATCCATAGCTGAGTGCATCTCTGTCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Qy 551 TGTGTGAATGTTTCTACAGAGCCCGAGGCGGTAAAGATTTCTTATTAAGATATCGGA 610
Db 538 TGTGTGAATGTTTCTACAGAGCCGTGAGGCGGTAAAGATTTCTTATTAAGATATCGGA 597
Qy 611 ATGACCACAGAGAGGTGAGAGAGCCCTTTCAGAGGCGCTTCGATGATGACAGCAAG 670
Db 598 ATGGCCACAGAGAGGTGAGAGAGCCCTTTCAGAGGCGCTTCGATGATGAGCAAG 657
Qy 671 ACCTGACAGAGAGTGTCCATCACTGTGCTCAAGTCACTGATGAGAGTCTGGCCCTACGA 730
Db 658 ACCTGACAGAGAGTGTCCATCACTGTGCTCAAGTCACTGATGAGAGTCTGGCCCTACGA 717
Qy 731 CCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTGTGAAAGACGAGC 790
Db 718 CATGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTGTGAAAGACGAGC 777
Qy 791 GGCTGATCCCTTAAAGTCAACCGAGAGGCTGAGAGAGACTTCACTGTGTGTCTAG 850
Db 778 GACTGATACCTTGTGAGTCACTGAAAGAGGCGGAGAGAGTTCACCTCGGTGTCTGG 837
Qy 851 AAATCATATGATGATCACTCTGTGCTCTCAACCTGTGTGCTGATGAGATAT 910
Db 838 AAATCATATGATGATCACTCTGTGCTCTCAACCTGTGTGCTGATGAGATAT 897
Qy 911 ATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
Db 898 ATTGCTACAGAAAGTCTCTAAAGCCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
Qy 971 TTGCTATCCCTTCAGAGAACAGAGAACTCTGTGTGTGATGAGAGATA 1009
Db 958 TTGCTATCCCTTCAGAGAACAGAGAACTCTGTGTGTGATGAGAGATA 1009

RESULT 14

AAC90601
ID AAC90601 standard; cDNA; 645 BP.
XX
XX AAC90601;
AC 13-MAR-2001 (first entry)
XX
XX Rat sodium channel beta3 protein Alrx94h5 partial coding sequence.
DB Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
XX neurodegenerative disorder; mood disorder; muscle contraction; ss.
XX
XX Rattus sp.
OS
XX WO200069912-A1.
PN 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013144.
PF 14-MAY-1999; 99US-0134198P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA Curtis RAJ;
XX

DR WPI; 2001-122743/13.
XX New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
XX root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX
XX Claim 1; Page 40-41; 145pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX rat sodium channel beta3 protein, designated Altra94b5. This protein is
XX involved in the generation of pain and other sensory or perceptive nerve
XX impulses, in the establishment and endurance of mood, neurodegenerative
XX and sleep disorders, and in the control of muscle contraction, including
XX movements such as the heartbeat, digestion and vascular tone. The
XX sequences can be used in predictive medicine, screening and diagnostic
XX assays, and in pharmacogenomics
XX
SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;
Query Match 42.4%; Score 534.6; DB 5; Length 645;
Best Local Similarity 89.3%; Pred. No. 2e-133;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 376 ATGCTGCTTCAATATGATTTTCCCTGCTTCTCTGCTTATCTACTGAGTCACT 435
DB 1 ATGCTGCTTCAATATGATTTTCCCTGCTTCTCTGCTTATCTACTGAGTCACT 60
QY 436 GTCTGCTTCTCTGCTTCTGCTGGAAGTCCCTCGAGACGAGCCGCTGACGAGCC 495
DB 61 GTCTGCTTCTCTGCTTCTGCTGGAAGTCCCTCGAGACGAGCCGCTGACGAGCC 120
QY 496 ATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
DB 121 ATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 556 GAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
DB 181 GATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 616 CACGAGAGGTGAGAGCCCTTTCAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTG 675
DB 241 CACGAGAGGTGAGAGCCCTTTCAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 676 CAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
DB 301 CAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 736 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
DB 361 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 796 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
DB 421 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 856 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
DB 481 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 916 TACAGAAAGTCTCAAAAAGCCGAGAGGAGCCCAAGAAACGCTGCTGCTGCTGCT 975
DB 541 TACAGAAAGTCTCTAAAGCCGAGAGGAGCCCAAGAAACGCTGCTGCTGCTGCT 600
QY 976 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 601 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
RESULT 15
AAV86895 standard; cDNA; 471 BP.
XX
AC AAV86895;

XX
XX 27-APR-1999 (first entry)
XX
XX EST clone BM4.
DE
XX
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
XX tissue growth; actinin; inhibin; tumour invasion suppressor; EST; human;
XX chemotaxis; chemokinesis; hemostasis; gene therapy; thrombolysis;
XX receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
XX Homo sapiens.
XX
XX MO9845435-A2.
XX
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98MO-US006954.
XX
XX 10-APR-1997; 97US-00835913.
XX
XX (GEM) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Werberg D, Treacy M;
XX Spaulding V, Agoestino MJ;
XX
XX WPI; 1999-070076/06.
XX
XX New polynucleotides encoding human secreted proteins - derived from e.g.
XX human blood, kidney, foetal lung, placenta, testes, brain, ovary,
XX pituitary, retina and colon cDNA libraries.
XX
XX Claim 1; Page 383-384; 633pp; English.
XX
XX This sequence represents an expressed sequence tag (EST), and is a
XX polynucleotide of the invention. The polynucleotides of the invention are
XX all secreted EST sequences isolated from a variety of human tissue
XX sources. The EST sequences and proteins encoded by them are predicted to
XX have useful biological activities which would make them suitable for
XX treating, preventing or ameliorating medical conditions in humans and
XX animals, although no supporting data is given. Suggested activities
XX include nutritional activity, immune stimulating or suppressing activity,
XX haematopoiesis regulating activity, tissue growth activity,
XX actinin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity. The EST sequences are also stated to be useful for gene therapy
XX
SQ Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;
Query Match 34.0%; Score 429; DB 2; Length 471;
Best Local Similarity 99.5%; Pred. No. 4.7e-105;
Matches 440; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 369 CCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
DB 22 CCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 81
QY 429 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 488
DB 82 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 140
QY 489 CAACCCCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB 141 CAACCCCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
QY 549 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
DB 201 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260
QY 609 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
DB 261 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320

| | | | |
|----|-----|--|-----|
| OY | 669 | GGACCTGCAGACGTCCTCATCTGTGCTCAACGTCACTCTGAACGACTTGACCTCTA | 728 |
| Db | 321 | GGACCTGCAGACGTCCTCATCTGTGCTCAACGTCACTCTGAACGACTTGACCTCTA | 380 |
| OY | 729 | CACCTGCATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAC | 788 |
| Db | 381 | CACCTGCATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAC | 440 |
| OY | 789 | GGGCTGATCCCCCTAAGATC | 810 |
| Db | 441 | GGGCTGATCCCCCTAAGATC | 462 |

Search completed: April 1, 2005, 19:02:57
 Job time : 767 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 18:37:20 ; Search time 245 Seconds

(without alignments)
8421.816 Million cell updates/sec

Title: US-09-977-579-4

Perfect score: 1261
Sequence: 1 cccctccctccgcagctcagc.....tgcacagactgagagccgcg 1261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 143.8 | 11.4 | 617 | 4 | US-09-949-016-2369 |
| 2 | 51 | 4.0 | 11174 | 4 | US-09-949-016-1411 |
| 3 | 48.6 | 3.9 | 30337 | 4 | US-09-949-016-13053 |
| 4 | 45.4 | 3.6 | 1645 | 4 | US-09-023-587A-5 |
| 5 | 44.8 | 3.6 | 11558 | 5 | PCT-US93-06251-23 |
| 6 | 44.8 | 3.6 | 13706 | 4 | US-09-902-540-1124 |
| 7 | 44.8 | 3.6 | 2133 | 4 | US-09-902-540-4106 |
| 8 | 42.4 | 3.4 | 23738 | 4 | US-09-902-540-1203 |
| 9 | 42.4 | 3.3 | 9622 | 4 | US-09-949-016-15003 |
| 10 | 42 | 3.3 | 666 | 4 | US-09-469-039A-3591 |
| 11 | 41.6 | 3.3 | 2943 | 4 | US-09-902-540-3929 |
| 12 | 40.6 | 3.2 | 21295 | 4 | US-09-902-540-1194 |
| 13 | 40.6 | 3.2 | 1533 | 4 | US-09-902-540-7877 |
| 14 | 40.4 | 3.2 | 5228 | 4 | US-09-902-540-4944 |
| 15 | 40.4 | 3.2 | 6651 | 4 | US-09-902-540-1243 |
| 16 | 40.4 | 3.2 | 30780 | 4 | US-09-949-016-1335 |
| 17 | 40.4 | 3.2 | 2806 | 4 | US-09-688-1888-102 |
| 18 | 40.2 | 3.2 | 2806 | 4 | US-09-291-417D-102 |
| 19 | 40.2 | 3.2 | 2838 | 4 | US-09-949-016-794 |
| 20 | 40.2 | 3.2 | 57559 | 4 | US-09-949-016-13077 |
| 21 | 40.2 | 3.2 | 57560 | 4 | US-09-949-016-12536 |
| 22 | 40.2 | 3.1 | 601 | 4 | US-09-949-016-124631 |
| 23 | 39.2 | 3.1 | 732 | 4 | US-09-902-540-3806 |
| 24 | 39.2 | 3.1 | 6202 | 4 | US-09-774-528-120 |
| 25 | 39.2 | 3.1 | 8374 | 4 | US-09-949-016-15257 |
| 26 | 39.2 | 3.1 | 8374 | 4 | US-09-949-016-15257 |
| 27 | 39.2 | 3.1 | 8374 | 4 | US-09-949-016-15257 |

| | | | | | | | |
|---|----|------|-----|-------|---|---------------------|--------------------|
| C | 28 | 39.2 | 3.1 | 18551 | 4 | US-09-902-540-1187 | Sequence 1187, Ap |
| C | 29 | 39.2 | 3.1 | 45225 | 4 | US-09-949-016-12428 | Sequence 12428, A |
| C | 30 | 39.2 | 3.1 | 45226 | 4 | US-09-949-016-13654 | Sequence 13654, A |
| C | 31 | 39.2 | 3.1 | 30635 | 4 | US-09-949-016-16501 | Sequence 16501, A |
| C | 32 | 39.2 | 3.1 | 43414 | 4 | US-09-949-016-16891 | Sequence 16891, A |
| C | 33 | 39.2 | 3.1 | 43415 | 4 | US-09-949-016-16891 | Sequence 16891, A |
| C | 34 | 38.8 | 3.1 | 1941 | 4 | US-09-902-540-4762 | Sequence 4762, Ap |
| C | 35 | 38.8 | 3.1 | 26492 | 4 | US-09-902-540-1234 | Sequence 1234, Ap |
| C | 36 | 38.6 | 3.1 | 513 | 4 | US-09-902-540-8812 | Sequence 8812, Ap |
| C | 37 | 38.6 | 3.1 | 1407 | 4 | US-09-902-540-6215 | Sequence 6215, Ap |
| C | 38 | 38.6 | 3.1 | 1940 | 4 | US-09-718-032-1 | Sequence 1, Appl |
| C | 39 | 38.6 | 3.1 | 1941 | 3 | US-09-082-737-1 | Sequence 1, Appl |
| C | 40 | 38.6 | 3.1 | 2310 | 4 | US-09-774-528-142 | Sequence 142, Appl |
| C | 41 | 38.6 | 3.1 | 6242 | 4 | US-09-949-016-16490 | Sequence 16490, A |
| C | 42 | 38.6 | 3.1 | 8122 | 4 | US-09-902-540-937 | Sequence 937, Ap |
| C | 43 | 38.6 | 3.1 | 1332 | 4 | US-09-902-540-1047 | Sequence 1047, Ap |
| C | 44 | 38.6 | 3.1 | 32495 | 4 | US-09-949-016-14952 | Sequence 14952, A |
| C | 45 | 38.4 | 3.0 | 505 | 4 | US-09-621-976-15639 | Sequence 15639, A |

ALIGNMENTS

| | | | | | | | |
|---|-----|--|-----|-----|--|-----|--|
| RESULT 1 | | | | | | | |
| US-09-949-016-2369 | | | | | | | |
| Sequence 2369, Application US/09949016 | | | | | | | |
| Patent No. 6812339 | | | | | | | |
| GENERAL INFORMATION: | | | | | | | |
| APPLICANT: VENTER, J. Craig et al. | | | | | | | |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | | | | | | | |
| FILE REFERENCE: C1001307 | | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/949, 016 | | | | | | | |
| CURRENT FILING DATE: 2000-04-14 | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/241, 755 | | | | | | | |
| PRIOR FILING DATE: 2000-10-20 | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/237, 768 | | | | | | | |
| PRIOR FILING DATE: 2000-10-03 | | | | | | | |
| PRIOR APPLICATION NUMBER: 60/231, 498 | | | | | | | |
| PRIOR FILING DATE: 2000-09-08 | | | | | | | |
| NUMBER OF SEQ ID NOS: 207012 | | | | | | | |
| SOFTWARE: FastSeq for Windows Version 4.0 | | | | | | | |
| SEQ ID NO 2369 | | | | | | | |
| LENGTH: 617 | | | | | | | |
| TYPE: DNA | | | | | | | |
| ORGANISM: Human | | | | | | | |
| US-09-949-016-2369 | | | | | | | |
| Query Match | | | | | | | |
| Best Local Similarity 56.9%; Pred. No. 36-31; | | | | | | | |
| Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3; | | | | | | | |
| QY | 441 | CTTCCTGTCGTGTGTAAGTGCCTTCGAGACGAGCCGTCAGGCAACCCATGAA | 500 | 11 | CTCAGGGGGGCTGCTGAGAGTGCCTCGAGACCGAGCCGCTGATGAGATGCA | 70 | |
| QY | 501 | GCTCCGCTGATCTCTCATGAAGAGAGAGAGTGAAGCCACGCTGTGATG | 560 | 71 | AATCTTTGATCTCTCGAGCGCCGAGACCAACGCTGAGACCTTCACCGAGTG | 130 | |
| QY | 561 | GTTCTACAGCGCCGAGGGGCTAAAGATT-----TCCTATTAGAGATGGAA | 611 | 131 | GACCTTCGCGACAGAGGCACTGAGAGTTGTCAAGATCTCGCTATGAGATGAGT | 190 | |
| QY | 612 | TGCGACCAAGAGAGAGAGCCCTTTCAGAGGGCCCTGCAAGTGAATGCGAG----- | 665 | 191 | GTTGAGAGCTGAG | 250 | |
| QY | 666 | ---CAAGAGCTGAG | 722 | 251 | CACCAAGAGCTGAG | 310 | |
| QY | 723 | CCCTACAGCTGAG | 782 | | | | |

Db 311 CCACTACAGAGTCCAGCTCTACCGCTGCTTTCTTCGAAAACACTGAGACACACACCG 370
Qy 763 GACGACGGGGGCTGATCCCTTAAGAGTACCGAGAGGTGAGAGACTTACCTCTGT 842
Db 371 CGTCCTCAAGAAATCCACATTTAGAGTGTGACAAAGCAACAGAGCATGCTCCAT 430
Qy 843 GGTCTCAGAAATCATGATGATGATCATCTTCTGTCTTCTTCACCTGTGGCTGCTCATGA 902
Db 431 CGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
Qy 903 GATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAG--GAGCCCAAGAAAGCC 959
Db 491 GATGATTTACTGCTACAGAAAGATGCTGCGCCGACGAGAGTCTGACAGAGAAATGC 550
Qy 960 GCTGCTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1006
Db 551 CTGGAATATCTGCGCATCATCTCTGAAAGCAAGAAAGAACTGACGCG 597

RESULT 2

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

Query Match 4.0%; Score 51; DB 4; Length 11174;

Best Local Similarity 58.1%; Pred. No. 0.00076;

Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 441 CTTCCCTGTGTGTGTGAAGTCCCTCGAGAGCGAGCGCTGACGGGCAACCCATGAA 500
Db 2011 CTGCGGGGGCTGCTGAGAGTGAAGTCCGAGACCGAGCGCGTGTATGGATGACCTTCAA 2070
Qy 501 GGTGGGCTGATCTCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
Db 2071 AATTTCTTTCATCTCTGCAAGCGCGCGAGCGAGCAACAGCTTGAGACCTTCAACGAGG 2130
Qy 561 GTTCTACAGGCCCGAGGGGCGTAAAGATTTCCTTA 595
Db 2131 GACCTTCCGCCAGAGGGGCACTGAGAGATTGTCA 2165

RESULT 3

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 3.9%; Score 48.6; DB 4; Length 30337;

Best Local Similarity 63.0%; Pred. No. 0.0062;

Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 829 GACTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
Db 620 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
Qy 889 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 947
Db 680 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 738

RESULT 4

US-09-023-587A-5
; Sequence 5, Application US/09023587A
; Patent No. 6653530
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K.
; APPLICANT: Bhal, Ganesh B.
; APPLICANT: Venkatramesh, Mylavartapu
; APPLICANT: Rangwala, Shaikat H.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Boddupalli, Sekhar S.
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,
; TITLE OF INVENTION: Specialty Oils in Plant Seeds
; FILE REFERENCE: 16516.122
; CURRENT APPLICATION NUMBER: US/09/023,587A
; CURRENT FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
US-09-023-587A-5

Query Match 3.6%; Score 45.4; DB 4; Length 1645;

Best Local Similarity 46.2%; Pred. No. 0.012;

Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 429 GGTAGTGTCTGCTTCCCTGT 488
Db 349 GGTGTCAAGCGGCTTCTTCTTAAGGTACAGGCGCCAAAGCGGCAAGCGCTGTACGT 408
Qy 489 CAACCCATGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 548
Db 409 GGTGCTACCAACACTGACGAGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
Qy 549 GGTGTGAGATGTGTTCTTACAGGCGCGGAGGCGGTAAGATTCTTATTATTCAGAGATCG 608

Db 469 CGAGTGAACGCGATGCTGGGCGCGAGCGGCCAACTCTCGCTGGCCAAACAGATGG 528
Qy 609 GAATGCCACCCAGAGAGTGAAGAGCCCTTTACAGGGCGCGCTGAGTGAATGGACCA 668
Db 529 CGGGGCGACTACGAGTACGCGCATCGGTTCCAGAGCGCGGTAAAGATCCCGACACAA 588
Qy 669 GGACCTGCAAGAGAGCTGCTCATCTGCTGCAAGTCACTGACGACTCTGGCTCTA 728
Db 589 GATGCTGACTACGAGAGAGCGCGCGAGATGTACGTGCGGACGACTCTCTCCGACTT 648
Qy 729 CACTGCAATGTGTCCCGGAGTTGA 755
Db 649 CTACGGCTGGGTGTCCCGAAGTGA 675

RESULT 5
US-09-902-540-2666
Sequence 2666, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2666
LENGTH: 1053
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2666

Query Match 3.6%; Score 44.8; DB 4; Length 1053;
Best Local Similarity 52.1%; Pred. No. 0.014;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 436 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGAGCGAGCGCGTGCAGGCAACCC 495
Db 151 GACTTCTCCACGAGACCTGCTGAGACTGCGCTCGAAGATGACGAGCGGACCCACTC 210
Qy 496 ATGAAGCTGGCTGATCTCTGATGAAGAGAGAGAGGTGAGGCGCACCGAGTGTG 555
Db 211 ATCCACCGGCTGGTGGCTTCTTCCGACGCGTGAAGCATGCTGCGCAACACTGTG 270
Qy 556 GAATGTTCTACAGCGCCGAGCGCGGTAAAGATTCTTATTCAGATTCGGAATGC 615
Db 271 CTGAACCTTACAGACCTGAACGCGCCCTGAAGCGCGGATGTACTGTGCGCCAGCTC 330
Qy 616 CACGAGAGGTG 627
Db 331 TACGAGAGGCG 342

RESULT 6
PCT-US93-06251-23
Sequence 23, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
NUMBER OF SEQUENCES: 93
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11558 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-23

Query Match 3.6%; Score 44.8; DB 5; Length 11558;
Best Local Similarity 56.7%; Pred. No. 0.048;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 74 GGGGTGGGCGGGAGGCGACTGTCGCTGTGCTGAGCGCGCGGAGCGGGCGGAGC 133
Db 428 GGGAGGGGCGGGTGGAGGACCTTTCAGAGCAGAGAGGCTTTGGGGCGTGGCGCGC 487
Qy 134 GCGTGTGCGCTTCTCGAAGTGGAGGTTCAGTGGGTG-CTTAGGGCCCAAGCCC 192
Db 488 TGGGAGCGGAGCGGGCTCGACGCGGTGCGCTGCGCGCGAGTGTATGACAGCGCGC 547
Qy 193 CCACCGGCTCCCAAGCTTCCAGGGCTTCCAGAGCAGCGGTGCTGCGCTTCTTCG 252
Db 548 CCGGCGGAGACCCCGAGCGCGCGGCTTCCACCGCGCGGCTTCCCGCG 607

RESULT 7
US-09-902-540-1124/c
Sequence 1124, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1124
LENGTH: 13706
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1124

Query Match 3.6%; Score 44.8; DB 4; Length 13706;
Best Local Similarity 52.1%; Pred. No. 0.052;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 436 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGAGCGAGCGCGTGCAGGCAACCC 495
Db 4948 GACTTCTCCACGAGACCTGCTGAGACTGCGCTCGAAGATGACGAGCGGAGCGCACCTC 4889

OY 496 ATGAAGCTCGCTGCATCTCTGATGAAGAGAGAGGTGGAGCCACCAAGTGTG 555
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
Db 4888 ATCCACCGGCTGTGGCGCTTCTTCCGACGGGTGACAGATCGTGGCAACAACCTGGTG 4829
OY 556 GAATGCTTCTACAGCCCGGAGGCGGTAAAGATTCTTATTAGAGTATGGAAATGGC 615
Db 4828 CTGAACCTCTACAAACACCTGAACGCCCTGTAGGCGGAGTGTACTGTGCGCCAGCTC 4769
OY 616 CACGAGAGGTG 627
Db 4768 TACGAGAGGCG 4757

RESULT 8
US-09-902-540-4106/c

; Sequence 4106, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4106
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4106

Query Match 3.4%; Score 42.4; DB 4; Length 2133;
Best Local Similarity 51.6%; Pred. No. 0.1;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

OY 462 GCCCTCGAGAGAGGCGCGTGCAGAGGCAACCCCAATGAAGTGGCTGCATCTCTGCAT 521
Db 1813 GCCCAGATGATGGCGGGCGCCCATCCCTTGAAGACGCTGCAAGCGCCGCTGCHG 1754
OY 522 GAAGAGAGAGAGAGTGAAGTGAAGCCACCAAGTGTGATGTTCTACAGGCGCGAGGCGG 581
Db 1753 GAAGCGGGCGGCGAGTGGAGACAGCTGGCGCTGGGACCGCTTCCAGACCAAGTGTGT 1694
OY 582 TAAAGATTCTTATTATTCAGATATCGAATGCGCAACCAAGAGGTGAGAGCCCTTTCA 641
Db 1693 GGGTGAACGCTCCGCTACGAGATCTGCGGAGCTCGGACAGCGCGCGTGC 1634
OY 642 GGGGCGCC 649
Db 1633 GCTCCGCC 1626

RESULT 9

US-09-902-540-1203
; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203

; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203

Query Match 3.4%; Score 42.4; DB 4; Length 23738;
Best Local Similarity 51.6%; Pred. No. 0.34;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

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Db 4191 GCCCAGATGATGGCGGGCGCCCATCCCTTGAAGACGCTGCAAGCGCCGCTGCHG 4250
OY 522 GAAGAGAGAGAGTGAAGTGAAGCCACCAAGTGTGATGTTCTACAGGCGCGAGGCGG 581
Db 4251 GAAGCGGGCGGCGAGTGGAGACAGCTGGCGTGGACCGCTTCCAGACCAAGTGTGT 4310
OY 582 TAAAGATTCTTATTATTCAGATATCGAATGCGCAACCAAGAGGTGAGAGCCCTTTCA 641
Db 4311 GGGTGAACGCTCCGCTACGAGATCTGCGGAGCTCGGACAGCGCGCGTGC 4370
OY 642 GGGGCGCC 649
Db 4371 GCTCCGCC 4378

RESULT 10

US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SBO ID NO 15003
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15003

Query Match 3.3%; Score 42; DB 4; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

OY 38 GAGCGAGCGAGGCGCGTGAAGTGAAGTTCGGGGTGGCGGAGGCGAAGTGTG 97
Db 7138 GCGTAGGCGCTGCTGAAGAGGGGTGCTGCTGCGGTAGGGGTCTGTTCATAGCCACGA 7079
OY 98 CGTGTGCTAGAGCGCGCGGAGAGCGGCGGAGAGCGGCTTATGAGCTTCTTCAACTGG 157
Db 7078 TCTGCTGCTGTGTGGGCGGAGCGCGGTGTAGGAAGCATATGCTTCCATGCGGTGG 7019
OY 158 GGAGGTCCAGTGGGGTGTGCTTAAGGCGCAAGCCGCCAGCGGCTCCAAAGCTCCAGG 217
Db 7018 ACAGGACCTTGGGGGCAAGTGAAGCTTCAACCCCTGGCTGTGACAGCCCTCCAGC 6959
OY 218 GCTTCCAGGACACGAGTGTCTGCGCCCTTCTTCTGCGTC 255
Db 6958 TACACCCAGCAGCTCCCTTCTGATCTCTTGGAC 6921

RESULT 11

US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIORITY FILING DATE: 2000-01-27
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

Query Match 3.3%; Score 41.6; DB 4; Length 696;
Best Local Similarity 48.3%; Pred. No. 0.098;
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 458 AAGTGCCTCGAGACGAGCGCGTGCAGGCAACCCATGAAGCTGCGTGCATCTCT 517
DB 92 AGGCGCGCAGCTCGCGCAGCGCGTGTGCGCAAGCTGCCGAGCCGCGCTATGCGGACT 151
QY 518 GCATGAAGAGAGAGGTGAGAGCCACACGCTGTGTAATGTTCTACAGCCCGAGG 577
DB 152 ACCTGCGCTTCAACGAGTGAAGGTAACCCGCTGATCAAGGGAATTCGCTGTGTTCC 211
QY 578 GCGGTAAGATTCTTATTATGAGATGCAATGAGCCACGAGAGGTGAGAGCCCTT 637
DB 212 CCGGCGCGAATCTCTTACCGGGAGAGATGTCTTAAGCTGCGAGGCGACGCGGCCG 271
QY 638 TTCAGGCGCGCTGAGTGAATGAGCAAGGACCTGCGAGAGCTGTCCATCTGTGC 697
DB 272 TCATTCTGACCTGTGCTTAACGTAATTCGACCCGCGCGGCGCTGCGATGCGCAGG 331

RESULT 12
US-09-902-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIORITY FILING DATE: 2001-07-10
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929
; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match 3.2%; Score 40.6; DB 4; Length 2943;
Best Local Similarity 48.9%; Pred. No. 0.39;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGAGACGAGCGCGTGCAGGCAACCCATGAAGCTGCGTGCATCTCTGC 519
DB 1831 GTGCTGGAAGAGGTGAGAGCGCGCTGCGCGAGCTGCGCTATGCGCGAGAGCCCG 1890
QY 520 ATGAAGAGAGAGGTGAGAGCCACACGCTGTGTAATGTTCTACAGCCCGAGGCG 579
DB 1891 ATGGCTTACGCGCAGAGCTGAAGGCCCGGTGAGAGCGCGCGCCCGCAGGTGAAGCGC 1950

QY 580 GGTAAAGATTCTTATTACAGATATCGAATGSCACAGAGGTGAGAGCCCTT 639
DB 1951 GCTTATGACCCGCTCTCGAGCTGCGCAGCTTGTACCGCGCCCGGTGAGCCCTGTG 2010
QY 640 CAGGCGCGCTGAGTGAATGAGCAGCAGGACCTGACGAGC 682
DB 2011 AAGCGCGCCAGAGAGGCAATGGCATGAGAGCCGAGAGAGG 2053

RESULT 13
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIORITY FILING DATE: 2001-07-10
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194

Query Match 3.2%; Score 40.6; DB 4; Length 21295;
Best Local Similarity 48.9%; Pred. No. 1.1;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGAGACGAGCGCGTGCAGGCAACCCATGAAGCTGCGTGCATCTCTGC 519
DB 2609 GTGCTGGAAGAGGTGAGAGCGCGCTGCGCGAGCTGCGCTATGCGCGAGAGCCCG 2668
QY 520 ATGAAGAGAGAGGTGAGAGCCACACGCTGTGTAATGTTCTACAGCCCGAGGCG 579
DB 2669 ATGGCTTACGCGCAGAGCTGAAGGCCCGGTGAGAGCGCGCCCGCAGGTGAAGCGC 2728
QY 580 GGTAAAGATTCTTATTACAGATATCGAATGSCACAGAGGTGAGAGCCCTT 639
DB 2729 GCTTATGACCCGCTCTCGAGCTGCGCAGCTTGAACCGCGCGGTGAGCGCTGTG 2788
QY 640 CAGGCGCGCTGAGTGAATGAGCAGCAGGACCTGACGAGC 682
DB 2789 AAGCGCGCCAGAGAGGCAATGGCATGAGAGCCGAGAGAGG 2831

RESULT 14
US-09-902-540-7877
; Sequence 7877, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIORITY FILING DATE: 2001-07-10
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7877
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

US-09-902-540-7877

Query Match 3.2%; Score 40.4; DB 4; Length 1533;
Best Local Similarity 47.9%; Pred. No. 0.32;
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY CGGAATGGCCACAGAGAGTGGAGAGCCCTTTCAAGGGCGCTGACAGTGAATGACAGC 666
DB CGGATGCCCCGAGACAGTGTGCTCCGAGGAGGGGCTGTCTCGGGGATGGGAGC 369
QY AAGAACCTGACAGAGTGTCCATCACTGTCTCAACGTCACTTGAACGACTTGGCCTC 726
DB ACGGAGCTGACAGAGCTGTGGCGCGGTACCAAGGTGAACGCGCTGGGTCCACGTGGGC 429
QY TACACCTGCAATGTGTCCCGGAGTTTGAAGTTGAGCGCATCGGCCCTTGTGAAGACG 786
DB TTGACCCGACCCCATGCGCGGTGGCTCTGTGAAGGGGCGCTGGCGAACGTGGGCATCAC 489
QY 787 ACGCGGCTGATCCCTTAAGATCACGAGAGAGCTGAGAGGACTTCACTGTGGTGC 846
DB GTGCTGTGCGGCTGTCTGTCTTCAACGCGGGGCGCTTCTGTGTCAGCGCGGCATCGTG 549
QY 847 TC 848
DB 550 TC 551

RESULT 15

US-09-902-540-789
Sequence 789, Application US/09902540

; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 789
; LENGTH: 5228
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-789

Query Match 3.2%; Score 40.4; DB 4; Length 5228;
Best Local Similarity 47.9%; Pred. No. 0.6;

Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY CGGAATGGCCACAGAGAGTGGAGAGCCCTTTCAAGGGCGCTGACAGTGAATGACAGC 666
DB CGGATGCCCCGAGACAGTGTGCTCCGAGGAGGGGCTGTCTCGGGGATGGGAGC 3116
QY AAGAACCTGACAGAGTGTCCATCACTGTCTCAACGTCACTTGAACGACTTGGCCTC 726
DB ACGGAGCTGACAGAGCTGTGGCGCGGTACCAAGGTGAACGCGCTGGGTCCACGTGGGC 3176
QY TACACCTGCAATGTGTCCCGGAGTTTGAAGTTGAGCGCATCGGCCCTTGTGAAGACG 786
DB TTGACCCGACCCCATGCGCGGTGGCTCTGTGAAGGGGCGCTGGCGAACGTGGGCATCAC 3236
QY 787 ACGCGGCTGATCCCTTAAGATCACGAGAGAGCTGAGAGGACTTCACTGTGGTGC 846
DB GTGCTGTGCGGCTGTCTGTCTTCAACGCGGGGCGCTTCTGTGTCAGCGCGGCATCGTG 3296
QY 847 TC 848
DB 3297 TC 3298

Search completed: April 1, 2005, 21:58:17
Job time : 252 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 20:37:33 ; Search time 816 Seconds
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9353.177 Million cell updates/sec

Title: US-09-977-579-4

Perfect score: 1261
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5607317 seqs, 302624599 residues

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Minimum DB seq length: 0

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Maximum Match 100%
Listing first 45 summaries

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Published Applications NA:
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21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1261 | 100.0 | 1261 | 11 | US-09-977-579-4 |
| 2 | 559.6 | 44.4 | 2632 | 13 | US-10-029-191-22 |
| 3 | 559.6 | 44.4 | 3108 | 11 | US-10-029-191-1 |
| 4 | 540 | 42.8 | 2220 | 11 | US-09-977-579-3 |
| 5 | 534.6 | 42.4 | 645 | 13 | US-10-029-191-21 |
| 6 | 216 | 17.1 | 4625 | 10 | US-09-764-891-7659 |
| 7 | 148.2 | 11.8 | 657 | 13 | US-10-029-191-23 |
| 8 | 143.8 | 11.4 | 1335 | 18 | US-10-723-860-2247 |
| 9 | 142.2 | 11.3 | 1414 | 18 | US-10-477-272-1 |
| 10 | 141 | 11.2 | 407 | 17 | US-10-276-774-718 |
| 11 | 138.6 | 11.0 | 1490 | 9 | US-09-917-800A-1654 |

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|----|------|-----|--------|----|----------------------|-------------------|
| 12 | 81.4 | 6.5 | 807 | 17 | US-10-401-916-12 | Sequence 12, Appl |
| 13 | 81.4 | 6.5 | 974 | 17 | US-10-401-916-13 | Sequence 13, Appl |
| 14 | 49 | 3.9 | 243 | 16 | US-10-029-386-16214 | Sequence 16214, A |
| 15 | 49 | 3.9 | 569 | 16 | US-10-029-386-2514 | Sequence 2514, Ap |
| 16 | 48.6 | 3.9 | 3583 | 18 | US-10-723-860-6471 | Sequence 6471, Ap |
| 17 | 45.4 | 3.6 | 876 | 18 | US-10-767-701-10747 | Sequence 10747, A |
| 18 | 45.2 | 3.6 | 497 | 17 | US-10-424-599-133788 | Sequence 133788, |
| 19 | 45.2 | 3.6 | 954 | 18 | US-10-425-115-100998 | Sequence 100998, |
| 20 | 44.8 | 3.6 | 921 | 17 | US-10-369-493-43050 | Sequence 43050, A |
| 21 | 44.8 | 3.6 | 29340 | 18 | US-10-322-281-642 | Sequence 642, App |
| 22 | 43.8 | 3.5 | 1434 | 17 | US-10-259-194A-622 | Sequence 622, App |
| 23 | 43.8 | 3.5 | 1720 | 17 | US-10-425-114-15213 | Sequence 15213, A |
| 24 | 43.8 | 3.5 | 1764 | 17 | US-10-425-114-15538 | Sequence 15538, A |
| 25 | 43.8 | 3.5 | 1794 | 17 | US-10-425-114-25057 | Sequence 25057, A |
| 26 | 43.8 | 3.5 | 2029 | 18 | US-10-425-115-15884 | Sequence 15884, A |
| 27 | 43 | 3.4 | 396 | 18 | US-10-437-963-98256 | Sequence 98256, A |
| 28 | 43 | 3.4 | 1021 | 18 | US-10-767-701-11876 | Sequence 11876, A |
| 29 | 42.8 | 3.4 | 1298 | 18 | US-10-437-963-21288 | Sequence 21288, A |
| 30 | 42.6 | 3.4 | 419 | 18 | US-10-425-115-24179 | Sequence 24179, A |
| 31 | 42.2 | 3.3 | 1211 | 18 | US-10-437-963-27585 | Sequence 27585, A |
| 32 | 41.6 | 3.3 | 1362 | 17 | US-10-282-122A-23492 | Sequence 23492, A |
| 33 | 41.4 | 3.3 | 686 | 18 | US-10-437-963-90177 | Sequence 90177, A |
| 34 | 41.4 | 3.3 | 58038 | 19 | US-10-741-600-17942 | Sequence 17942, A |
| 35 | 41.4 | 3.3 | 333811 | 19 | US-10-741-600-17681 | Sequence 17681, A |
| 36 | 41.2 | 3.3 | 922 | 15 | US-10-017-161-1435 | Sequence 1435, Ap |
| 37 | 41.2 | 3.3 | 922 | 17 | US-10-292-798-1161 | Sequence 1161, Ap |
| 38 | 41 | 3.3 | 1097 | 9 | US-09-771-161A-58 | Sequence 58, Appl |
| 39 | 41 | 3.3 | 3382 | 9 | US-09-771-161A-59 | Sequence 59, Appl |
| 40 | 40.6 | 3.2 | 221000 | 17 | US-10-174-014-12 | Sequence 12, Appl |
| 41 | 40.6 | 3.2 | 23380 | 13 | US-10-087-192-652 | Sequence 652, App |
| 42 | 40.2 | 3.2 | 766 | 17 | US-10-260-238-52 | Sequence 52, Appl |
| 43 | 40.2 | 3.2 | 779 | 17 | US-10-425-114-26163 | Sequence 26163, A |
| 44 | 40.2 | 3.2 | 791 | 18 | US-10-437-963-84059 | Sequence 84059, A |
| 45 | 40.2 | 3.2 | 1071 | 18 | US-10-437-963-84064 | Sequence 84064, A |

ALIGNMENTS

RESULT 1
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129, 473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match 100.0%; Score 1261; DB 11; Length 1261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CCTCTCCCTCCGAGCTGAGCTTACCTCTGCGGAAACGAGCGGAGCGGCGGAGTGG 60
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721 GGCCTCTTACACCTGAGATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCTTTTGTG 780
781 AAGACGAGCGGCTGATCCCTTAAGAGTCCAGGAGGCTGAGAGGAGCTTCACTCT 840
781 AAGACGAGCGGCTGATCCCTTAAGAGTCCAGGAGGCTGAGAGGAGCTTCACTCT 840
841 GTGTCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 GTGTCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCGGAGAGGCGCCCAAGAAAACCG 960
901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCGGAGAGGCGCCCAAGAAAACCG 960
961 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCGGAGAGGCGCCCAAGAAAACCG 960
961 GAGATGATATATTTGCTACAGAAAGTCTCAAAAAGCGGAGAGGCGCCCAAGAAAACCG 960
1021 TAGAACAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1021 TAGAACAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1081 TTACGCAATGTCAATGAGATCAGAGAGGCGCCCAAGGCGCCCATGCTTCCCTTCAATG 1140
1081 TTACGCAATGTCAATGAGATCAGAGAGGCGCCCAAGGCGCCCATGCTTCCCTTCAATG 1140
1141 ATTCATGTGTCTGCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200
1141 ATTCATGTGTCTGCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200

1201 GACTCCCTAATCTCATCAGACCTCTACGACCATTAAGACTCTGCGAGAACTGAGAGCCG 1260
1201 GACTCCCTAATCTCATCAGACCTCTACGACCATTAAGACTCTGCGAGAACTGAGAGCCG 1260
1261 G 1261
1261 G 1261
1261 G 1261
RESULT 2
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00X/501
; CURRENT APPLICATION NUMBER: US/10/029.191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22
Query Match 44.4%; Score 559.6; DB 13; Length 2632;
Best Local Similarity 84.4%; Pred. No. 3.1e-163;
Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;
371 AGAAGATCCCTGCTCAATGATGTTTCCCTGAGCTTCTCTGCTTACTACTGAG 430
73 AAAAGATCCCTGCTCAACAGATTTGCTTCCCTGAGCTTCTCTGCTTACTACTGAG 132
431 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
133 TCAGTGTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
491 ACCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
193 ATCCCATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 252
551 TGTGGAATGCTTCTACAGGCGCGAGGCGGTAAGATTTCTTATTTACGATACGGA 610
253 TGTGGAATGCTTCTACAGGCGCGAGGCGGTAAGATTTCTTATTTACGATACGGA 312
611 ATGGCCACAGAGGTGAGAGCCCTTTTACAGGGCGCTGCAAGTGAATGGCAAGAGG 670
313 ATGGCCACAGAGGTGAGAGCCCTTTTACAGGGCGCTGCAAGTGAATGGCAAGAGG 372
671 ACCCTGAGAGAGTGTCTCATCTGTGCTCAACGTCATCTGAAAGACTCTTGGCTCTTCA 730
373 ACCCTGAGAGAGTGTCTCATCTGTGCTCAACGTCATCTGAAAGACTCTTGGCTCTTCA 432
731 COTGCAATGTGTCCCGGAGGTTTGTGAGGGCATCGGCGCTTGTGAAGAGCAGC 790
433 CATGCAATGTGTCCCGGAGGTTTGTGAGGGCATCGGCGCTTGTGAAGAGCAGC 492
791 GCGTGAATCCCTTAAGAGTCAACGAGAGGCTGAGAGAGCTTCACTCTGTGTCTGAG 850
493 GACTGATATCTTTGGAGTCACTGAAGAGGCGGAGGAACTTCACTCTGTGTCTGAG 552
851 AAATCATATGTAATCTTCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 910
553 AAATCATATGTAATCTTCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 612

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QY      911  ATTGCTACAGAAAGSTCTCTCAAAAGCCGGAAGAGGACGCCAGAAAACCGTCTGATCAC 970
Db      613  ATTGCTACAGAAAAGTCTCTTAAAGCCGGAAGAGGACGACAGAAAATTCGTTGACTAAC 672
QY      971  TTGCGATCCCATCTGAGAAACAAGAGAACTGTGCGGTACACAGTGGAGGAATAGAAACAGA 1030
Db      673  TTGCTATTCCTTACAGAGAAACAAGAGAACTGTGTGTACTCTGTGAGGAAATG-----AT 726
QY      1031 GCAGTGTGACATGAGAGTGGCCCTGAACACCTGAGGAGACTGGAATCCATGTTTCAGCAATG 1090
Db      727  GTGGTGTGACTTGAAGTGTACTGTG-AGTGTGAGGAGACTGAGTATTCCTCCAGTTCAGTGATG 785
QY      1091 TCATGTGCATGAGAGGCGCGCCCAAGGCCCCCATCGTCTTCCCTTCATGCATCCAT 1146
Db      786  CCAGCAATATACAGGAAGTGGCCCCCAGGTGTCCCAACATCATCATCTTTTCTATTCAAT 841

RESULT 3
US-10-029-191-1
/ Sequence 1, Application US/10029191
/ Publication No. US20020160453A1
/ GENERAL INFORMATION:
/ APPLICANT: CURTIS, ROY A.J.
/ TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
/ TITLE OF INVENTION: PROTEIN
/ FILE REFERENCE: 210147.00X/5U1
/ CURRENT APPLICATION NUMBER: US/10/029.191
/ CURRENT FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 09/569,978
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/134,198
/ PRIOR FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 3108
/ TYPE: DNA
/ ORGANISM: Rattus sp.
/ US-10-029-191-1

```

| Query Match | 44.4% | Score 559.6 | DB 13 | Length 3108 |
|-----------------------|----------------|---|----------|-------------|
| Best Local Similarity | 84.4% | Pred. No. 3.3e-163 | | |
| Matches 655 | Conservative 0 | Mismatches 114 | Indels 7 | Gaps 2 |
| QY | 371 | AGAAAGTGCCTGCCTTCATAGATTGTTTCCCTGGCTTCTCTCGTCTTACTAGG | 430 | |
| Db | 73 | AAAGAGTCCGCTTCAACAGATTGCTTCCCTAGCTTCTAGTGTCTACTAGG | 132 | |
| QY | 431 | TCAATGTCGTTTCCCTGTGTGTGTGGAAGTCCCTCGAAGCGAGGCCGTGCAGGCA | 490 | |
| Db | 133 | TCAAGTGTGTTCCCTGTGTGTGTGGAAGTCCCTCGAAGCGAGGCCGTGCAGGCA | 192 | |
| QY | 491 | ACCCATGAAGCTCGCTGCATCTCTCTCATGAAGAGAGAGAGGTGAGGCCACACAG | 550 | |
| Db | 193 | ATCCATGAAGCTAGTGATCTCTCTCATGAAGAGAGAGAGGTGAGGCCACACAG | 252 | |
| QY | 551 | TGTGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGATACGA | 610 | |
| Db | 253 | TGTGTGAATGTTCTACAGGCCCTGAGGGCGGTAAAGATTTCCTTATTTACGATACGA | 312 | |
| QY | 611 | ATGACCAACAGAGAGTGAAGAGCCCTTTCAGGGCGGCTCAGTGAATGGACAGAG | 670 | |
| Db | 313 | ATGACCAACAGAGAGTGAAGAGCCCTTTCAGGGCGGCTCAGTGAATGGAGCAAG | 372 | |
| QY | 671 | ACCTGCAGAGAGTGTCCATCACTGTGTCTCAAGCTCATCTTGAAAGCATCTTGACCTTACA | 730 | |
| Db | 373 | ACCTGCAGAGAGTGTCCATCACTGTGTCTCAAGCTCATCTTGAAAGCATCTTGACCTTACA | 432 | |
| QY | 731 | CCTGAATGTGTCCCGGAGATTGTGATTGAGGCGCATCGGCCCTTTGTAAGACGAGC | 790 | |
| Db | 433 | CATGAATGTGTCCCGGAGATTGTGATTGAGGCGCATCGGCCCTTTGTAAGACGAGC | 492 | |
| QY | 791 | GGCTGATCCCTTAAGATCAACGAGAGCGCTGAGAGAGACTTCACTGTGTCTCAG | 850 | |

Db 493 GACTGATACCTTTTCCGAGTCACTGTAAGGGCGGAGAACTTACCTCCGTGGCTTCGG 552
 Qy 851 AAATCATGATGATACATCCTTCTGGTCTTCTCTCAACCCTGGGCTGCTCATCGAGATGATAT 910
 Db 553 AAATCATGATGATACATCCTCCTGGTCTTCTCTCAACTTGTGGCTGTTATTGATGATGATCT 612
 Qy 911 ATTGCTACAGAAAGCTCTCAAAAAGCCGAAGAGGAGGCCCAAGAAAAGCGCTGTGACTATCC 970
 Db 613 ATTGCTACAGAAAGCTCTTAAGGCCGGAAGAGGCGAGACAGAAAATGCGCTGTACTATCC 672
 Qy 971 TTGCTATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCAAGTGTAGAGAAATAGAAACAGA 1030
 Db 673 TTGCTATCCCTTCAGAGAAACAAGAGAACTCTGTGTATACCTGTGTAGAGAAATA-----AT 726
 Qy 1031 GCACTGTGACATGAGGTGGCGCTGAAACACTGAGGGACTGGAATCCCATGTTTCGCAATG 1090
 Db 727 GTGTGTGTGACTGTGAGGTGATCTG-AGTGCTGAGGGAATGGAATATCCCAAGTTCAGTATG 785
 Qy 1091 TCATGTGATAGAGAGGGGCGCCCAAGAGGCCCAATGCGTTCCCTTCATGATCATCAT 1146
 Db 786 CCACGAAATATCAGGAAGTGGCCCAAGGTGTCCCAACAATCATCATCTTTTCTATTTAT 841

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RESULT 4
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses th
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

```

| | Query Match | 42.8%; | Score 540; | DB 11; | Length 2220; |
|----|-----------------------|--|---------------------|-----------|--------------|
| | Best Local Similarity | 89.3%; | Pred. No. 3.7e-157; | | |
| | Matches 582; | Conservative 0; | Mismatches 70; | Indels 0; | Gaps 0; |
| Qy | 371 | AGAGATGCGCCCTTCATATGATTTGTTCCCTCGGCTTCTCTGTGCTTATCTACTGGG | 430 | | |
| Db | 358 | AAAAGATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTATCTACTGGG | 417 | | |
| Qy | 431 | TCAGTGTCTGCTTCCCTGTGTGTGTGAGAGTGCCCTCGAGACGAGCGCTGCAGGCA | 490 | | |
| Db | 418 | TCAGAGTCTGCTTCCCTGTGTGTGTGTGAGAGTGCCCTCGAGACAGAAACGATGCAGGGCA | 477 | | |
| Qy | 491 | ACCCCATGAAGCTGCGCTGCATCTTCCTGCATGAAGAAGAGAGAGTGAAGGCCACACAGG | 550 | | |
| Db | 478 | ATCCCATGAAGCTGAGGTGCATCTTCCTGCATGAAGAAGAGAGAGTGAAGGCCACCACTG | 537 | | |
| Qy | 551 | TGTGTGAATGTTTACAGGCCGAGGGCGGTAAAGATTTCCTTAATTACAGATATGCGA | 610 | | |
| Db | 538 | TGTGTGAGTGTCTTACAGGCTCTGAGGCGGTAAAGATTTCCTTAATTATGAGATATGCGA | 597 | | |
| Qy | 611 | ATGTCACACAGAGAGTGTGAGAGCCCTTTTACAGGGGCCCTTGCAATGTGATATGGCCAGAG | 670 | | |
| Db | 598 | ATGTCACACAGAGAGTGTGAGAGCCCTTTTCCAGGGCGCTTGCAATGTGATATGGAGCAAG | 657 | | |
| Qy | 671 | ACCTGCAGAGACTGTTCATCACTGTGTCTCAACGTCACTTGAAAGCACTTGCGCTCTACA | 730 | | |

Db 658 ACCTCAGAGACGATTCACATCTACATCAATGATCACTTGAATCACTCGCCCTTACA 717
Qy 721 CCTGAATGTGTCGGGGAGTTGAGTTGAGGCGCATCGCCCTTGTGAAGAGAGCGC 790
Db 718 CATTGAATGTGTCGGGGAGTTGAGTTGAGGCGCATCGCCCTTGTGAAGAGAGCGC 777
Qy 721 GAGTATCCCTTGAAGAGTTGAGTTGAGGCGCATCGCCCTTGTGAAGAGAGCGC 850
Db 778 GACTATACCTTTGGAGTCACTGAAGAGGCGGGAAGACTTCACTCGGTCGCG 837
Qy 851 AATGATGATGATCACTCTTGTGTTCTTCACTCGGTCGCTCATCGATGATAT 910
Db 838 AATGATGATGATCACTCTTGTGTTCTTCACTCGGTCGCTCATCGATGATAT 897
Qy 911 ATTGCTACGAAAGGCTTCAAAAGCGGGAAGAGGCGGCAAGAAAGCGCTGACTACC 970
Db 898 ATTGCTACGAAAGGCTTCAAAAGCGGGAAGAGGCGGCAAGAAAGCGCTGACTACC 957
Qy 971 TTGCAATCCCATCTGAGAACAGAGAACTCTGCGTACAGTGGAGGATA 1022
Db 958 TTGCAATCCCATCTGAGAACAGAGAACTCTGCGTACAGTGGAGGATA 1009

RESULT 5
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIORITY FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match 42.4%; Score 534.6; DB 13; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.1e-155;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 376 ATGCTGCTTCAATAGATGTTTCCCTGCTTCTCTGCTTATCTACTGCGTCACT 435
Db 1 ATGCTGCTTCAATAGATGTTTCCCTGCTTCTCTGCTTATCTACTGCGTCACT 60
Qy 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTGAGAGAGAGCGCGTCAAGAGAGAGCC 495
Db 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTGAGAGAGAGCGCGTCAAGAGAGAGCC 120
Qy 496 ATGAAGCTGCGTGTGATCTCTGATGAAGAGAGAGAGTGTGAGGCAACCACTG 555
Db 121 ATGAAGCTGAGGTGATCTCTGATGAAGAGAGAGAGTGTGAGGCAACCACTG 180
Qy 556 GAATGCTTCTACAGCCCGGAGGCGGTAAAGTTCTTATTTACGATATGCAATGCC 615
Db 181 GATGCTTCTACAGCCCGGAGGCGGTAAAGTTCTTATTTACGATATGCAATGCC 240
Qy 616 CACGAGAGAGTGAAGAGCCCTTGAAGGAGCGCTGAGTGAAGAGAGAGAGAGCTG 675
Db 241 CACGAGAGAGTGAAGAGCCCTTGAAGGAGCGCTGAGTGAAGAGAGAGAGAGCTG 300
Qy 676 CAGAGAGTGTCCATCACTGTGTGCTCAAGCTCACTGAAAGCACTGAGCTTACACTGC 735
Db 676 CAGAGAGTGTCCATCACTGTGTGCTCAAGCTCACTGAAAGCACTGAGCTTACACTGC 735

Db 301 CAGAGAGTATCATCACTGATCAATGTCACCTTGAATGACTCTGCGCTTACACATGC 360
Qy 726 AATGATCCCGGAGAGTTGAGTTGAGGCGCATCGCCCTTGTGAAGAGAGAGCGCTG 795
Db 361 AATGATCCCGGAGAGTTGAGTTGAGGCGCATCGCCCTTGTGAAGAGAGAGCGCTG 420
Qy 796 ATCCCTTGAAGAGTCAAGAGAGGCGTGAAGAGAGAGTTCACCTCTGTGTGTTCAATC 855
Db 421 ATACCTTGGAGTCACTGAAGAGGCGGAGAGAGAGTTCACCTCTGTGTGTTCAATC 480
Qy 856 ATGATGTCATCTCTTGTGTTCTTCTCACTCTGTGTGCTGCTCATGATATATATTC 915
Db 481 ATGATGTCATCTCTTGTGTTCTTCTCACTCTGTGTGCTGCTCATGATATATATTC 540
Qy 916 TACAGAAAGTCTCAAAAGCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975
Db 541 TACAGAAAGTCTCAAAAGCGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 976 ATCCCATCTGAGAACAGAGAGAACTCTGCGTACAGTGGAGGAA 1020
Db 601 ATCCCATCTGAGAACAGAGAGAACTCTGCGTACAGTGGAGGAA 645

RESULT 6
US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7659
; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7659

Query Match 17.1%; Score 216; DB 10; Length 4625;
Best Local Similarity 100.0%; Pred. No. 3.9e-56;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1044 AGTGGCTTGAACACCTGAGAGAGTGAACATCCCATGTTCAAGATGCAATGGCATCG 1103
Db 33 AGTGGCTTGAACACCTGAGAGAGTGAACATCCCATGTTCAAGATGCAATGGCATCG 92
Qy 1104 GAGGAGCGCCCAAGAGGCGCCCATGCTTCCCTTCAATGATCATGTTGTCTCAATTCAT 1163
Db 93 GAGGAGCGCCCAAGAGGCGCCCATGCTTCCCTTCAATGATCATGTTGTCTCAATTCAT 152
Qy 1164 CATCATATCATCACTGCTCTGAGCTTTCACCTGATCTGATCTCCATCTCATGAGACT 1223
Db 153 CATCATATCATCACTGCTCTGAGCTTTCACCTGATCTGATCTCCATCTCATGAGACT 212
Qy 1224 CTACGACCATTAAGACTCTGCGAAGACTGAGAGCC 1259
Db 213 CTACGACCATTAAGACTCTGCGAAGACTGAGAGCC 248

RESULT 7
US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191

;; CURRENT FILING DATE: 2001-12-20
;; PRIOR APPLICATION NUMBER: 09/569,978
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/134,198
;; PRIOR FILING DATE: 1999-05-14
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 23
;; LENGTH: 657
;; TYPE: DNA
;; ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 11.8%; Score 148.2; DB 13; Length 657;
Best Local Similarity 57.7%; Pred. No. 2,6e-35;
Matches 333; Conservative 0; Mismatches 223; Indels 21; Gaps 3;

QY 451 TGTGTGAAATGCTCTCGAGAGCGAGCCGTGCAAGGCAACCCCATGAAGCTGCCTGC 510
DB TCGGTGAGGTGAGCTCGAGAGCGAGCCGTGACGGATGACCTTCAAAATTTCTGTGC 120
QY 511 ATCTCTGCAATGAAGAGAGAGGTGAGGCCACACGCTGTGGAATGTTCTACAG 570
DB 121 ATCTCTGCAAGGCGCGACGAGACCAAGCCGAGACCTTCAAGAGTGAACCTTCCG 180
QY 571 CCCGAGGCGGTAAAGATT-----TCCTATTAGAGATGCGAATGGCCACAG 621
DB 181 CAGAGGCGCTAGAGAGTTCTGACAGATCTGCGCTATAGACAGAGTGTGCAGCTG 240
QY 622 GAGGTGAGAGCCCTTTCAGAGGCGCGCTGCAATGAGATGCGAG-----CAGAGAC 672
DB 241 GAGGAGAGAGGCGCTTTCAGAGGCGCGCTGAGAGAGGCGAGCGGCGGCAACAGAGAC 300
QY 673 CTGCAAGAGCTGTTCATCTGCTGCTCAAGTCACTTGAACGACTGTGCTTACACC 732
DB 301 CTGCAAGAGCTGTTCATCTGCTGCTCAAGTCACTTGAACGACTGTGCTTACACC 360
QY 733 TGCATGTGTCGCGGAGTTGAGTTGAGGCGATGCGGCTTTGAGAGAGAGCGCG 792
DB 361 TGCATGTGTCAGCGCTGCTCTCTTGAACCTGAGAGCAACACAGCGTGTCAAG 420
QY 793 CTGATCCCCCTAAGAGTCAACCGAGAGGCTGAGAGACTTCACTTGTGTCTAGAA 852
DB 421 AAGATTCACCTGAGAGGTGTGAGCAAGGCCAACAGAGACATGGCATTCATCGTGTGAG 480
QY 853 ATCATATGTACATCTTCTGTCTCTGCTTCTGACCCCTGTGCTCATCGAGATGATAT 912
DB 481 ATCATATGTACATCTGCTCATCGTGTGTGACCATCTGCTCGTGGCGAGATGATGAT 540
QY 913 TGTCTACAGAAAGTCTTCAAAAGCCGAAAGAGCA---GCCAAGAAAAGCGTGTGACTAC 969
DB 541 TGTCTACAGAAAGTCTTCAAAAGCCGCAAGAGCGCGGCAAGAGAGAGCGCTCGAGATAC 600
QY 970 CTGCGCATCCCATCTGAGAACAGAGAACTGTGCGG 1006
DB 601 TTGGCCATCCTCTCAGAAAGCAAAAGAAATTGACCG 637

RESULT 8
US-10-723-860-2247
;; Sequence 2247, Application US/10723860
;; Publication No. US20040253606A1
;; GENERAL INFORMATION:
;; APPLICANT: Aziz, Natascha
;; APPLICANT: Gineburg, Wendy M.
;; APPLICANT: Zlotnik, Albert
;; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
;; FILE REFERENCE: 05882.0193.NPUS01
;; CURRENT APPLICATION NUMBER: US/10/723,860
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: 60/429,739
;; PRIOR FILING DATE: 2002-11-26

;; NUMBER OF SEQ ID NOS: 8393
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2247
;; LENGTH: 1335
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-860-2247

Query Match 11.4%; Score 143.8; DB 18; Length 1335;
Best Local Similarity 56.9%; Pred. No. 7.8e-34;
Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3;

QY 441 CTTCCTGTGTGTGTAAGTGCCTTCGAGAGCGAGCCGTGCAAGGCAACCCCATGA 500
DB 75 CTGCGGGGCGTGTGTGAGGTGAGCTCGAGAGCGAGCCGTGTATGAGATGACCTTCAA 134
QY 501 GCTGCCCTGATCTCTGCAATGAAGAGAGGTGAGGCCACACGCTGTGGAATG 560
DB 135 AATCTTTGATCTCTGCAAGGCGCGAGCGAGACCAACGCTGAGACCTTCAACGAGTG 194
QY 561 GTTCTACAGCCCGAGGCGGTAAAGATT-----TCCTATTAGAGATGCGAA 611
DB 195 GACCTTCCGCAAGAGGCACTGAGAGTTGTCAAGATCTGCGCTATGAGATGAGT 254
QY 612 TGSCCAACAGAGAGTGAAGAGCCCTTTCAGAGGCGCGCTGCAATGAGATGAG 665
DB 255 GTTGCAAGTGAAGAGATGAGCGCTTTCAGAGGCGCGCTGTGATGAGATGAGCGG 314
QY 666 ---CAGAGACTGAGAGAGTGTTCATCACTGTGCTCAACGTGCACTTGAAGCACTTGG 722
DB 315 CACCAAGAGCTGAGAGATGTGTATCTTCACTCAACATGTCACCAACCACTCGGG 374
QY 723 CCTTACACTGTAATGTGTCCGAGAGTTGAGTTGAGGCCATCGGCTTTGAGAA 782
DB 375 CAGCTACAGATGCAAGTGTCAAGCTGCTCTTTCGAAAGTACAGAGCAACACAG 434
QY 783 GACGAGCGGCTGATCCCCCTAAGAGTCAACCGAGAGGCTGAGAGAGTCACTTGT 842
DB 435 CTGCTCAGAGAGATCACTTGAAGTGTGAGCAAAAGCCACAGAGATGAGCAT 494
QY 843 GGTCTCAGAAATCATGATGATCACTTCTGTCTTCTCAACCTGTGTGCTCATGCA 902
DB 495 CGTGTGAGATCATGATGATGATGCTCATGTGTGAGTGTGATGATGATGCTGTGAG 554
QY 903 GATGATATATGCTTCAAGAAAGTCTTCAAAAGCCGAAAGG---GCAAGCCAAAGAAAGCC 959
DB 555 GATGATATATGCTTCAAGAAAGTCTTCAAAAGCCGCAAGAGAGTGTGCAAGAGAGATG 614
QY 960 GTCTGACTACTTGCATCCCATCTGAGAACAGAGAACTGTGCGG 1006
DB 615 CTGGAATACCTGTGCTCATCACTTGAAGCAAAAGAACTGACCG 661

RESULT 9
US-10-477-272-1
;; Sequence 1, Application US/10477272
;; Publication No. US20040191791A1
;; GENERAL INFORMATION:
;; APPLICANT: Biomedics Limited
;; TITLE OF INVENTION: P12
;; FILE REFERENCE: SCN1B (P85C)
;; CURRENT APPLICATION NUMBER: US/10/477,272
;; PRIOR FILING DATE: 2003-11-10
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 1414
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-477-272-1
Query Match 11.3%; Score 142.2; DB 18; Length 1414;
Best Local Similarity 56.7%; Pred. No. 2.5e-33;

Matches 333; Conservative 0; Mismatches 233; Indels 21; Gaps 3;

```
OY 441 CTTCCTGTGTGTGTGAAGTCCCTCGAGACGAGGCGCTGACGGCAACCCCATGA 500
DB 151 CTGCGGGGGCTGCGGTGAGAGTGAAGTCCGAGACGAGGCGGTATGGAATACCTTCA 210
OY 501 GCTGCGCTGATCTCTCTGATGAAGAGAGAGAGTGAAGGACCAACGAGTGTGAATG 560
DB 211 AATCTTTGATCTCTCGAAGCGCGGACGAGACCAACGCTGAGACCTTACCGAGTG 270
OY 561 GTTCTACAGGCGCGGAGGCGGTAAAGATT-----TCCATTATTCGAGTATCGGA 611
DB 271 GACCTTCGCGCAAGAGGGGACCTGAGAGTGTTCAAAGTCTCGCCCTATGAAATGAGT 330
OY 612 TGGCCACGAGAGAGTGAAGGCGCTTTCAGAGGGGCGCTGACAGTGAATGCGAG----- 665
DB 331 GTTGAAGCTGAGAGAGATGAGTGTTCGAGGGCGCGCGGTGTGGAATGCGAGCGGGG 390
OY 666 ---CAAGACCTGACGAGAGCTGTCAATCACTGTGCTCAAAGTCACTGGAACGACTTGG 722
DB 391 CACCAAGACCTGACGAGATCTGTATCTTCAATCAACAAATGCACTTCAACACTCGGG 450
OY 723 CCTTACACCTGCAATGTGTCCCGGAGTTTGAAGTTGAGGGGCAATCGGCCCTTTGTGA 782
DB 451 GCACTACGAGTGCACGCTTACCGCGCTGCTTCTTTCGAAAACCTACGAGCAACACGAG 510
OY 783 GACGACGGGCTGATCCCGCTTAAGATCACCGAGAGGCTGAGAGAGACTTCACTCTGT 842
DB 511 CGTCTCAAGAGATCCCATTTGAGTGAAGTGAACAAAGCAACAGACATGGCATTCAT 570
OY 843 GGTCTCAAGAAATCATGATGATACATCTTCTGTCTTCTCTACCTGTGTGCTCATCGA 902
DB 571 CGTGTGAGATCATGATGTATGTGCTCATGTGTGATGACATATGGCTGTGAGAGA 630
OY 903 GATGATATTTGCTTCAAGAAAGTCTCAAAAGCCCAAGG---GACGCCAAGAAAAGCC 959
DB 631 GATGATTTTACGTCTCAAGAAAGATGCTGCGCGCACGAGACTGTGACACAGAGAATGC 690
OY 960 GCTGACTACCTTGGCATCCCATCTGAGAACAGAGAACTGTGCGG 1006
DB 691 CTCGAAATACCTGGCCATCATCTTGAAGCAAAAGAACTGACAGG 737

RESULT 10
US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718

Query Match 11.2%; Score 141; DB 17; Length 407;
Best Local Similarity 96.6%; Pred. No. 3.8e-33;
Matches 144; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 820 GCTGAGAGAGACTTCACTTGTGTGTGAGAAATCATGATGATACATCTTGTGTTCT 879
DB 220 GCTGAGAGAGACTTCACTTGTGTGTGAGAAATCATGATGATGATGATGATGATGAT 171
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OY 880 CTCACCTGTGTGCTGCTCATGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAA 939
DB 170 CTCACCTGTGTGCTGCTCATGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAA 111
OY 940 GAGGAGCCCAAGAAAGCGCTTGACTTA 968
DB 110 GAGGAGCCCAAGAAAGCGGTAAAGTCA 82
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RESULT 11
US-09-917-800A-1654
; Sequence 1654, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Caetle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1654
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654
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Query Match 11.0%; Score 138.6; DB 9; Length 1490;
Best Local Similarity 56.7%; Pred. No. 3.4e-32;
Matches 327; Conservative 0; Mismatches 229; Indels 21; Gaps 3;

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OY 451 TGTGTGAAGTCCCTCGGACGAGGCGCTGACAGGCAACCCCATGAAGTGGCGTC 510
DB 280 TGGTGAAGTGAATTTGAGACCGAGCGAGTATGGAATGACTTCAAAATCTGTGT 339
OY 511 ATCTCTCATGAAGAGAGAGAGTGAAGGACCAACGATGTGAATGTTCTTACAGG 570
DB 340 ATCTCTTGAAGCGCTGATGAGACCAACCGCGAGACCTTACGAGATGAGACTTCCG 399
OY 571 CCGAGGCGGTAAAGATT-----TCCATTATTCGATATCGAATGCGCACAG 621
DB 400 CAGAGGGGACAGAGAAATTTGTCAAGATCTTACGCTATGAAATGAGTGTGAGAGCTG 459
OY 622 GAGTGAAGAGCCCTTTCAAGGGGCGCTGCAATGGAATGGCAG-----CAAGAC 672
DB 460 GAGGAAGTGAAGCGCTTTGAGGGCGGTGTGATGGAACGAGTATGCGGGGACCAAGAG 519
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QY 673 CTCGAGACGCTGTCATCACTGCTCAAGCTCACTGTAACGACTGTGGCTCTACACC 722
 DB 520 CTCGAGACGCTGTCATCACTGCTCAAGCTCACTGTAACGACTGTGGCTCTACACC 579
 QY 733 TGCATGTCCTCCGAGGATTGAGTTGAGGCGCGCTCTTGTGAAGACGACGG 792
 DB 580 TGTACGCTACCGCTCTCTCTTGTGATTAACAGACCAACACGCGTGTCAAG 639
 QY 793 CTGATCCCTTAAGATCAACCGAGAGGCTGAGAGACTTCACTCTGTGTCTCAAG 852
 DB 640 AATATCCCTGAGAGGCTGAGAGGCTGAGAGACTTCACTCTGTGTCTCAAG 699
 QY 853 ATCATGATGATCACT 912
 DB 700 ATCATGATGATCACT 759
 QY 913 TGTACAGAAAGGCTCTCAAAAGCC--GAAAGGCGAGCCCAAGAAAGGCTGACTAC 969
 DB 760 TGTACAGAAAGGCT 819
 QY 970 CTGCGATCCCATCTGAGAACAGAGAACTCTGCGG 1006
 DB 820 CTGCGATCCCATCTGAGAACAGAGAACTCTGAG 856

RESULT 12

US-10-401-916-12
 ; Sequence 12, Application US/10401916
 ; Publication No. US20040002439A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Qln, Ning
 ; APPLICANT: Codd, Ellen
 ; APPLICANT: D'Andrea, Michael
 ; TITLE OF INVENTION: DNAs encoding human beta1a sodium channel subunit
 ; FILE REFERENCE: ORT-1221
 ; CURRENT APPLICATION NUMBER: US/10/401,916
 ; PRIOR FILING DATE: 2003-03-28
 ; PRIOR APPLICATION NUMBER: US/09/875,456A
 ; PRIOR FILING DATE: 2001-09-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 807
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-401-916-12

Query Match 6.5%; Score 81.4; DB 17; Length 807;
 Best Local Similarity 57.5%; Pred. No. 1,8e-14;
 Matches 195; Conservative 0; Mismatches 126; Indels 18; Gaps 2;

QY 441 CTTCCTGTGTGTGTGAGAGTGCCTTGAGAGCGAGCGCTGCAAGCCCATGAA 500
 DB 51 CTCGCGGGGGCTGCTGAGAGTGAAGCTCGAGACCGAGCGCTGATGAGATGACCTTCAA 110
 QY 501 GCTGCGCTGATCTCTGCTGTAAGAGAGAGAGTGAAGCCACCGTGTGAATG 560
 DB 111 AATCTTTTGTATCTCTGCAAGCGCGCGAGAGACCAAGCTGAGACCTTCAACCGAGTG 170
 QY 561 GTTCTACAGGCGCGGCGGTAAGAT-----TCCATTATTAAGATGAGAA 611
 DB 171 GACCTTCGCGCAAGAGGCACTGAGAGTTTTCAGATCTTCCGCTATAGAAATGAGT 230
 QY 612 TGGCCACCAAGAGAGTGAAGAGCCCTTTCAGGGGCGCTGCACTGAGTAAGTGGAG----- 665
 DB 231 GTTGCAGCTGAGAGAGATGAGCGCTTTCAGAGCGCGGCTGTGTGGAATGGACCGGGG 290
 QY 666 ---CAAGAGCTTGAAGAGAGTGTCACTGCTCAAGTCACTTGAAGCACTTGG 722
 DB 291 CACCAAGAGCTGAGAGATGTCTATCTTCACTCAACCAAGTCACTTCAACCACTCGGG 350
 QY 723 CCTCTACCTGCAATGTGTCCCGGAGTTGAGTTGA 761

DB 351 CGACTACGAGTGCACGCTTACCGCGCTCTCTTCTTGA 389

RESULT 13

US-10-401-916-13
 ; Sequence 13, Application US/10401916
 ; Publication No. US20040002439A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Qln, Ning
 ; APPLICANT: Codd, Ellen
 ; APPLICANT: D'Andrea, Michael
 ; TITLE OF INVENTION: DNAs encoding human beta1a sodium channel subunit
 ; FILE REFERENCE: ORT-1221
 ; CURRENT APPLICATION NUMBER: US/10/401,916
 ; PRIOR FILING DATE: 2003-03-28
 ; PRIOR APPLICATION NUMBER: US/09/875,456A
 ; PRIOR FILING DATE: 2001-09-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 974
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-401-916-13

Query Match 6.5%; Score 81.4; DB 17; Length 974;
 Best Local Similarity 57.5%; Pred. No. 1,9e-14;
 Matches 195; Conservative 0; Mismatches 126; Indels 18; Gaps 2;

QY 441 CTTCCTGTGTGTGTGAGAGTGCCTTGAGAGCGAGCGCTGCAAGCCCATGAA 500
 DB 54 CTCGCGGGGGCTGCTGAGAGTGAAGCTCGAGACCGAGCGCTGATGAGATGACCTTCAA 113
 QY 501 GCTGCGCTGATCTCTGCTGTAAGAGAGAGTGAAGCCACCGTGTGAATG 560
 DB 114 AATCTTTTGTATCTCTGCAAGCGCGCGAGAGACCAAGCTGAGACCTTCAACCGAGTG 173
 QY 561 GTTCTACAGGCGCGGCGGTAAGAT-----TCCATTATTAAGATGAGAA 611
 DB 174 GACCTTCGCGCAAGAGGCACTGAGAGTGTTCAGATCTTCCGCTATGAGATGAGT 233
 QY 612 TGGCCACCAAGAGAGTGAAGAGCCCTTTCAGGGGCGCTGCACTGAGTAAGTGGAG----- 665
 DB 234 GTTGCAGCTGAGAGAGATGAGCGCTTTCAGAGCGCGGCTGTGTGAATGGACCGGGG 293
 QY 666 ---CAAGAGCTTGAAGAGAGTGTCACTGCTCAAGTCACTTGAAGCACTTGG 722
 DB 294 CACCAAGAGCTGAGAGATGTCTATCTTCACTCAACCAAGTCACTTCAACCACTCGGG 353
 QY 723 CCTCTACCTGCAATGTGTCCCGGAGTTGAGTTGA 761
 DB 354 CGACTACGAGTGCACGCTTACCGCGCTGCTCTTCTTGA 392

RESULT 14

US-10-029-386-16214
 ; Sequence 16214, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
 ; FILE REFERENCE: AEOMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 16214
 ; LENGTH: 243
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: Q07699, EVALUE 5.00e-42
; OTHER INFORMATION: NT HIT: U12191.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF953777.1, EVALUE 1.00e-129
US-10-029-386-16214

Query Match 3.9%; Score 49; DB 16; Length 243;
Best Local Similarity 60.1%; Pred. No. 0.00014;
Matches 104; Conservative 0; Mismatches 60; Indels 9; Gaps 1;

OY 598 TACGATATCGGATGCGCAGGAGTGAGAGCCCTTCAGGGGCGCTGCAGTGG 657
DB 4 TATGAGATGAGGTGTGTCAGCTGAGAGGATGAGCCGCTTCAGGGCGCGGTGGTGG 63

OY 658 AATGCGAG-----CAGGACTGCGAGACGTGTCATCTGCTCAAGCTCACT 708
DB 64 AATGCGAGCGGGGCGACCAAGAGCCTGCGAGATCTGTCTTCTTCATCACCAATGTCAAC 123

OY 709 CTGAAGCACTGCGCTTACACCTGCAATGTCCTCCGGAGTTGAGTTGA 761
DB 124 TACAACCACTCGGGCGACTACAGATGCCAGTCTACCGCTGCTCTTTCGA 176

RESULT 15
US-10-029-386-2514

; Sequence 2514, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029.386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2514
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: Q07699, EVALUE 6.00e-42
; OTHER INFORMATION: NT HIT: U12191.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: B1754689.1, EVALUE 0.00e+00
US-10-029-386-2514

Query Match 3.9%; Score 49; DB 16; Length 569;
Best Local Similarity 60.1%; Pred. No. 0.00019;
Matches 104; Conservative 0; Mismatches 60; Indels 9; Gaps 1;

OY 598 TACGATATCGGATGCGCAGGAGTGAGAGCCCTTCAGGGGCGCTGCAGTGG 657
DB 62 TATGAGATGAGGTGTGTCAGCTGAGAGGATGAGCCGCTTCAGGGCGCGGTGGTGG 121
OY 658 AATGCGAG-----CAGGACTGCGAGACGTGTCATCTGCTCAAGCTCACT 708

DB 122 AATGCGAGCCGGGCGACCAAGAGCCTGCGAGATCTGTCTATCTTCATCACCAATGTCAAC 181
OY 709 CTGAAGCACTGCGCTTACACCTGCAATGTGTCGGGAGTTGAGTTGA 761
DB 182 TACAACCACTCGGGCGACTACAGATGCCAGCTTACCCGCTGCTTCTTTCGA 234

Search completed: April 1, 2005, 23:48:30
Job time : 823 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 18:32:30 ; Search time 4595 Seconds
(without alignments)
10445.929 Million cell updates/sec

Title: US-09-977-579-4

Sequence: 1 cccctccctccgcagctgagc.....ttgccagactgagagcccg 1261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|--------|-------------|-----------|----|----------------------|
| 1 | 1252.2 | 99.3 | 4052 | 3 | AL136589 Homo sapi |
| 2 | 909.4 | 72.1 | 2555 | 3 | CR609664 full-length |
| 3 | 768.6 | 61.0 | 1062 | 3 | EX420015 BX420015 |
| 4 | 652.6 | 51.8 | 975 | 5 | EX445002 BX445002 |
| 5 | 646.4 | 51.3 | 648 | 9 | AY419145 Homo sapi |
| 6 | 574 | 45.5 | 582 | 5 | BP202832 BP202832 |
| 7 | 567.8 | 45.0 | 582 | 5 | BP200910 BP200910 |
| 8 | 550.6 | 43.7 | 1359 | 3 | AK076466 Mus muscu |
| 9 | 542.6 | 43.0 | 3549 | 3 | AK049747 Mus muscu |
| 10 | 536.6 | 42.6 | 648 | 9 | AY419147 Mus muscu |
| 11 | 531.6 | 42.2 | 4149 | 3 | AK049286 Mus muscu |
| 12 | 524.4 | 41.6 | 672 | 2 | BB614118 BB614118 |
| 13 | 521.4 | 41.3 | 636 | 5 | BM933157 UT-M-BH3- |
| 14 | 514.2 | 40.8 | 4105 | 3 | BC058083 Mus muscu |
| 15 | 513 | 40.7 | 1078 | 1 | AL534136 AL534136 |
| 16 | 486.4 | 38.6 | 584 | 4 | BP361278 BP361278 |
| 17 | 473.6 | 37.6 | 950 | 4 | BG294174 BG294174 |
| 18 | 465 | 36.9 | 584 | 9 | AY419146 Pan trogl |
| 19 | 453.2 | 35.9 | 723 | 6 | CA749311 UT-M-PY0- |
| 20 | 447.2 | 35.5 | 927 | 5 | BO713131 AGNCOURT |
| 21 | 420.8 | 33.4 | 582 | 5 | BP311484 BP311484 |
| 22 | 397.4 | 31.5 | 1069 | 5 | BM928131 AGNCOURT |
| 23 | 390.8 | 31.0 | 825 | 5 | BO745919 UT-M-EX0- |
| 24 | 386.4 | 30.6 | 846 | 6 | CD355879 UT-M-PY0- |

| | | | | | | | |
|----|-------|------|-----|---|----------|----------|------------|
| 25 | 363.4 | 28.8 | 742 | 6 | CB526211 | CB526211 | UT-M-PY0- |
| 26 | 354 | 28.1 | 845 | 6 | CA327438 | CA327438 | UT-M-PY0- |
| 27 | 352.8 | 28.0 | 986 | 5 | BU118914 | BU118914 | 6031429291 |
| 28 | 349.2 | 27.7 | 700 | 4 | BT739617 | BT739617 | 603361873 |
| 29 | 348 | 27.6 | 975 | 5 | EX452112 | EX452112 | EX452112 |
| 30 | 347 | 27.5 | 692 | 7 | CN219870 | CN219870 | WLA010B08 |
| 31 | 341.8 | 27.1 | 652 | 2 | BB652801 | BB652801 | BB652801 |
| 32 | 332.4 | 26.4 | 892 | 5 | BU368614 | BU368614 | 603790206 |
| 33 | 326.4 | 25.9 | 595 | 5 | BU368531 | BU368531 | 603788820 |
| 34 | 310 | 24.6 | 450 | 6 | CB787935 | CB787935 | AMGNNUC:N |
| 35 | 307.2 | 24.4 | 712 | 6 | CB526257 | CB526257 | UT-M-PY0- |
| 36 | 306.2 | 24.3 | 734 | 7 | CK367344 | CK367344 | AGNCOURT |
| 37 | 305.2 | 24.2 | 780 | 5 | BO770528 | BO770528 | UT-M-PY0- |
| 38 | 303.6 | 24.1 | 823 | 7 | CO428866 | CO428866 | UT-M-PY0- |
| 39 | 297.2 | 23.6 | 750 | 6 | CD349206 | CD349206 | UT-M-PY0- |
| 40 | 294.2 | 23.3 | 895 | 5 | EX743834 | EX743834 | EX743834 |
| 41 | 287.2 | 22.8 | 714 | 7 | CF531573 | CF531573 | UT-M-PY0- |
| 42 | 273.4 | 21.7 | 669 | 5 | BM951151 | BM951151 | UT-M-PY0- |
| 43 | 269.8 | 21.4 | 471 | 6 | CB732717 | CB732717 | AMGNNUC:N |
| 44 | 264.4 | 21.0 | 705 | 6 | CD349958 | CD349958 | UT-M-PY0- |
| 45 | 256.8 | 20.4 | 798 | 7 | CF290312 | CF290312 | AGNCOURT |

ALIGNMENTS

RESULT 1
LOCUS HSM801563
DEFINITION Homo sapiens mRNA, cDNA DKFP761F182 (from clone DKFP761F182).
ACCESSION AL136589
VERSION AL136589.1 GI:13276680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4052)
Ottewaelder, B., Obermaier, B., Deutschenbur, S., Schaipe, A.,
Mewes, H.W., Weill, B., Amid, C., Oeanger, A., Fodo, G., Han, M. and
Wiemann, S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaeder Landstr. 1, D-85764
Neuerberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFP761F182) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneID=DKFP761F182
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="DKFP761F182"
/cissue_type="amygdala"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev stage="adult"
/note="voltage-gated sodium channel beta-3 subunit"
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/gene="DKFP761F182"
804..1451
/gene="DKFP761F182"
/codon_start=1
/product="hypothetical protein"

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/protein_id="CAB6524.1"
/db_xref="gi:13276681"
/db_xref="GOA:O9NY72"
/db_xref="UniProt/Swiss-Prot:O9NY72"
/translation="MPAFNRPLPLASLVLTIVSVCPVCVEPSEETAOVGNPKLR
CISCKREVEATVEMFYPREPKSLIYEYRNGHDEVSFPGRJQMGSKLQD
VSIPLVNTLNDGLYTCNVSRPEFEKRPVKTTRIPLATVEADEDFISVSEI
MMVILVFLTLMIETIYCYRKVSKAEBAQENSDYLAIPSEKENSAPVVEE"

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ORIGIN

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Query Match      99.3%; Score 1252.2; DB 3; Length 4052;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3  CTCCTTCGAGCTGAGCTTACCTCGGGCGCAACGAGGAGGCGAGGCGGAGTGA 62
431 CTCCTTCGAGCTGAGCTTACCTCGGGCGCAACGAGGAGGCGAGGCGGAGTGA 490
63  GCTGAGATTCCGGGGTGGGGGAGGCGAGCTGTCGTTGTTCTGAGCGCCGCGAGAGC 122
491 GCTGAGATTCCGGGGTGGGGGAGGCGAGCTGTCGTTGTTCTGAGCGCCGCGAGAGC 550
123 GGGCGCGAGGCGGCTGATGCGCTCCCTCGAATCGGAGAGGCTCAAGTGGGTTGCTTA 182
551 GGGCGCGAGGCGGCTGATGCGCTCCCTCGAATCGGAGAGGCTCAAGTGGGTTGCTTA 610
183 CCCAAGGCGCGCGAGCTCCAAAGCTCCAGGAGGCTCCCGAGGCAACGGTGTGCTGGC 242
611 CCCAAGGCGCGCGAGCTCCAAAGCTCCAGGAGGCTCCCGAGGCAACGGTGTGCTGGC 670
243 CCTTCCTTCGAGTCAAGAAAGTCCCGCTGGGGGCAAGTTCGCAAAAGGGTTTCCTGAA 302
671 CCTTCCTTCGAGTCAAGAAAGTCCCGCTGGGGGCAAGTTCGCAAAAGGGTTTCCTGAA 730
303 AGAATCTGAGAGGCGGCGAGCTCTTGAACGAGGAAATCTTCTGTGTAGTGGCTTGAAGCCG 362
721 AGAATCTGAGAGGCGGCGAGCTCTTGAACGAGGAAATCTTCTGTGTAGTGGCTTGAAGCCG 790
363 CCAGGCGCGAGAGTGGCTGCTCAATAGATTGTTCCCTGGGCTTCTGTGTGCTTAT 422
791 CCAGGCGCGAGAGTGGCTGCTCAATAGATTGTTCCCTGGGCTTCTGTGTGCTTAT 850
423 CTACTGGGTCAAGTGTCTGCTTCCCTGTGTGTGTGAGAGTGGCCCTCGAGAGCGAGCCGT 482
851 CTACTGGGTCAAGTGTCTGCTTCCCTGTGTGTGTGAGAGTGGCCCTCGAGAGCGAGCCGT 910
483 GAGGCGCAACCCCATGAGAGTGGCTGCTTCTTCTGCAAGAGAGAGAGAGTGAAGGC 542
911 GAGGCGCAACCCCATGAGAGTGGCTGCTTCTTCTGCAAGAGAGAGAGAGTGAAGGC 970
543 CACCAAGGAGTGGAGTGTCTCAAGGCGCGAGGCGGCTAAAGATTCTTATTATTAAGA 602
971 CACCAAGGAGTGGAGTGTCTCAAGGCGCGAGGCGGCTAAAGATTCTTATTATTAAGA 1030
603 GATTCGGAATGGCCACGAGAGGTGAGAGCCCTTTCAAGGCGCGCTTCACTGGAATGG 662
1031 GATTCGGAATGGCCACGAGAGGTGAGAGCCCTTTCAAGGCGCGCTTCACTGGAATGG 1090
663 CAGCAAGAGCTGTCAGAGAGTGTCCATCACTGTGCTCAACGTCATCTTGAAGACTCTGG 722
1091 CAGCAAGAGCTGTCAGAGAGTGTCCATCACTGTGCTCAACGTCATCTTGAAGACTCTGG 1150
723 CCTTACACCTGCAATGTGTCCCGGAGATTGAGTTGAGGGGCAATCGGCCCTTTGTGA 782
1151 CCTTACACCTGCAATGTGTCCCGGAGATTGAGTTGAGGGGCAATCGGCCCTTTGTGA 1210
783 GACGAGCGGCTGATCCCTTAAGAGTCAACGAGAGGCTGAGAGAGACTTCAACCTCTGT 842
1211 GACGAGCGGCTGATCCCTTAAGAGTCAACGAGAGGCTGAGAGAGACTTCAACCTCTGT 1270
843 GGTCTCAGAAATCATGATGTACATCTTGTGTTCTTCTCAACCTGTGGCTCTCATCGA 902
1271 GGTCTCAGAAATCATGATGTACATCTTGTGTTCTTCTCAACCTGTGGCTCTCATCGA 1330

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QY 903 GATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAAGCGCTC 962
DB 1331 GATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAAGCGCTC 1390
QY 963 TGACTTACTTGGCATCCCATCTGAGACAGAGAGAACTTGTGGTTCACAGTGGAGAAATA 1022
DB 1511 CAGCAATGTCAATGAGCATCAGAGAGGCGCCCAAGGCGCCCATGCTTCCCTTCATGAT 1570
QY 1143 CCATTGTTCTGTTCAATTCATTCATCAATCAATCCACTGCTTGAAGCTTTCACCTCTGA 1202
DB 1571 CCATTGTTCTGTTCAATTCATTCATCAATCAATCCACTGCTTGAAGCTTTCACCTCTGA 1630
QY 1203 CTCCTTAATCCTCAGACCTCTACGACCATTAAGACTCTGCGAGAACTGAGAAAGCC 1259
DB 1631 CTCCTTAATCCTCAGACCTCTACGACCATTAAGACTCTGCGAGAACTGAGAAAGCC 1687

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RESULT 2
CR609664 2555 bp mRNA linear HTC 21-JUL-2004
LOCUS CR609664
DEFINITION Full-length cDNA clone CS0DF023YA09 of Fetal Brain of Homo sapiens
(human).
ACCESSION CR609664
VERSION CR609664.1 GI:50490471
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2555)
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2555)
REFERENCE
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-Ligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1..2555
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF023YA09"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"

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FEATURES

source

ORIGIN

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Query Match      72.1%; Score 909.4; DB 3; Length 2555;
Best Local Similarity 99.9%; Pred. No. 4,2e-225;
Matches 910; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 349 AGCTTTGAGAGCGCGCAGCGCCAGAGAGTCCCTGCTTCATATAGATTGTTCCCTGGCT 408
DB 208 AGCTTTGAGAGCGCGCAGCGCCAGAGAGTCCCTGCTTCATATAGATTGTTCCCTGGCT 267

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| | | | |
|----|------|---|------|
| QY | 409 | CTCTCGAGCTTATATACCTGGGTCAGTGCTTCCTCCGTGTGTGTAAGTGGCCCTCG | 468 |
| Db | 268 | TCTCTCGTCTTATTACTGGGTCAAGTGTCTCTCTCTGTGTGTGTAAGTGGCCCTCG | 327 |
| QY | 469 | GAGACGAGGCCGTGTGCAAGGCAACCCCATGAAGCTTCGCTGCATCTCTGCATGAAGAGA | 528 |
| Db | 328 | GAGACGAGGCCGTGTGCAAGGCAACCCCATGAAGCTTCGCTGCATCTCTGCATGAAGAGA | 387 |
| QY | 529 | GAGAGGTGAGAGGCCCAACGGTGGTGGAAATGGTCTCTACAGGCCCCGAGAGGCGGTAAAGAT | 588 |
| Db | 388 | GAGAGGTGAGAGGCCCAACGGTGGTGGAAATGGTCTCTACAGGCCCCGAGAGGCGGTAAAGAT | 447 |
| QY | 589 | TTCTCTTATTTACGAGTATCGAATGCGCACACGAGAGTGTAGAGCCCTTTTCAGGGCGC | 648 |
| Db | 448 | TTCTCTTATTTACGAGTATCGAATGCGCACACGAGAGTGTAGAGCCCTTTTCAGGGCGC | 507 |
| QY | 649 | CTGCAGTGGAAATGGGACGAAAGAACCTGCAAGACGTGTCCATATCTGTGTCAAGTCACT | 708 |
| Db | 508 | CTGCAGTGGAAATGGGACGAAAGAACCTGCAAGACGTGTCCATATCTGTGTCAAGTCACT | 567 |
| QY | 709 | CTGAACGACTCTGGGCTCTACACCTCGCAATGTATCCCGGAGTTTGAGTTTGAAGCGCAT | 768 |
| Db | 568 | CTGAACGACTCTGGGCTCTACACCTCGCAATGTATCCCGGAGTTTGAGTTTGAAGCGCAT | 627 |
| QY | 769 | CGGCCCTTTTGTGAAGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGAGGCTGGAAG | 828 |
| Db | 628 | CGGCCCTTTTGTGAAGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGAGGCTGGAAG | 687 |
| QY | 829 | GACTTCAACCTCTGAGTCTCAAGAAATCAATGATGTATCATCTTCTGTCTTCTCAACCTG | 888 |
| Db | 688 | GACTTCAACCTCTGAGTCTCAAGAAATCAATGATGTATCATCTTCTGTCTTCTCAACCTG | 747 |
| QY | 889 | TGGCTGTCTCATCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGACACC | 948 |
| Db | 748 | TGGCTGTCTCATCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGACACC | 807 |
| QY | 949 | CAAGAAAACGGGTCTGACTTACCTTGGCCATCCCATTTGAGAACAGAGAGAACTCTTCGGTA | 1008 |
| Db | 808 | CAAGAAAACGGGTCTGACTTACCTTGGCCATCCCATTTGAGAACAGAGAGAACTCTTCGGTA | 867 |
| QY | 1009 | CCAGTGTGAGAAATGAAACAGAGACAGTGTGACATGAGGTGGGCTTGAACACTGAGGAGACT | 1068 |
| Db | 868 | CCAGTGTGAGAAATGAAACAGAGACAGTGTGACATGAGGTGGGCTTGAACACTGAGGAGACT | 927 |
| QY | 1069 | GGAACATCCCATGTTTCAGCAATGTCAATGGCATCAGAGAGGCGGCCCAAGAGGCCCATGCG | 1128 |
| Db | 928 | GGAACATCCCATGTTTCAGCAATGTCAATGGCATCAGAGAGGCGGCCCAAGAGGCCCATGCG | 987 |
| QY | 1129 | TTCCCTTATGATCATCCATTTGTTCTGTTGATTCATTCATCCATACATCCACCTGGCTCTGA | 1188 |
| Db | 988 | TTCCCTTATGATCATCCATTTGTTCTGTTGATTCATTCATCCATACATCCACCTGGCTCTGA | 1047 |
| QY | 1189 | GCTTTCACCTCTGACTCCCTTAACCTCCATCAGACCTTACGCAACCAATGAAGACTTGCAGA | 1248 |
| Db | 1048 | GCTTTCACCTCTGACTCCCTTAACCTCCATCAGACCTTACGCAACCAATGAAGACTTGCAGA | 1107 |
| QY | 1249 | ACTGAGGAAGCC 1259 | |
| Db | 1108 | ACTGAGGAAGCC 1118 | |

| RESULT 3 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM |
|----------|---|--|-----------|---------|----------|--------|----------|
| BX420015 | BX420015 | 1062 bp mRNA | | | | | |
| | BX420015 | Homo sapiens FETAL BRAIN Homo sapiens CDNA clone | | | | | |
| | CSDDF023YK09.5-PRIME | mRNA sequence. | | | | | |
| | BX420015 | | | | | | |
| | BX420015.2 | GI:46929710 | | | | | |
| | EST. | | | | | | |
| | Homo sapiens (human) | | | | | | |
| | Homo sapiens | | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | | |

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|---------------------|---|--|--------------------|--|
| 1 (bases 1 to 1062) | Li, W. B., Gruber, C., Jessee, J. and Polayes, D. | Full-length cDNA libraries and normalization | Unpublished (2001) | On May 13, 2003 this sequence version replaced gi:30646738 |

Genoscope - Centre National de Séquençage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqlife@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS0DF023A0A50Q1&c=6147.r>.

FEATURES

SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODF0237A09"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_1ib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer; five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

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|---------------------------|-------|---------------------|-----------|--------------|
| Query Match | 61.0% | Score 768.6; | DB 5, | Length 1062; |
| Best Local Similarly | 93.0% | Pred. No. 1.4e-188; | | |
| Matches 797; Conservative | 15; | Mismatches 44; | Indels 1; | Gaps 1 |

| | | | |
|----|-----|--|-----|
| Oy | 349 | AGCCTTGGAAACCGCAGACCGCCAGAAATGCTGCCTTCATTAATGTTTCCCTGGCT | 408 |
| Db | 207 | AGCCTTGGAAACCGCAGACCGCCAGAAATGCTGCCTTCATTAATGTTTCCCTGGCT | 266 |
| Oy | 409 | TCTCTCGTCTTAATCTAAGTGTGATGCTCTTCCCTGTGTGTGAAATGCTCCCTCG | 468 |
| Db | 267 | TCTCTCGTCTTAATCTAAGTGTGATGCTCTTCCCTGTGTGTGAAATGCTCCCTCG | 326 |
| Oy | 469 | GAGACGAGAGCCGTGACAGGCGCAACCCCATGAAGCTGGCTCATCTCTGCATGAAGAGA | 528 |
| Db | 327 | GAGACGAGAGCCGTGACAGGCGCAACCCCATGAAGCTGGCTCATCTCTGCATGAAGAGA | 386 |
| Oy | 529 | GAGAGGTGAGGCGCACCGGTGTGAAATGTTCTACAGGCCCGAGGCGGTAAAGAT | 588 |
| Db | 387 | GAGAGGTGAGGCGCACCGGTGTGAAATGTTCTACAGGCCCGAGGCGGTAAAGAT | 446 |
| Oy | 589 | TTCTCTTAATTTACGAGTATCCGAAATGGAGCCACAGAGGGTGAAGAGCCCTTTCAAGGGGCGC | 648 |
| Db | 447 | TTCTCTTAATTTACGAGTATCCGAAATGGAGCCACAGAGGGTGAAGAGCCCTTTCAAGGGGCGC | 506 |
| Oy | 649 | CTGCAGTGAATGCGAGCAAGATCTGCGAGAGCTGTCCATCACTGTGCTCAACGTCAT | 708 |
| Db | 507 | CTGCAGTGAATGCGAGCAAGATCTGCGAGAGCTGTCCATCACTGTGCTCAACGTCAT | 566 |
| Oy | 709 | CTGAACGACTTGGCCTTCTACACTGCAATGTGTCCGGAGATTGAACTTTGAAGCCGAT | 768 |
| Db | 567 | CTGAACGACTTGGCCTTCTACACTGCAATGTGTCCGGAGATTGAACTTTGAAGCCGAT | 626 |
| Oy | 769 | CGGCGCTTTTGAAGAAGACGCGGCTGATCCCTTAAGAATCAACCGAGAGGCTGGAAG | 828 |
| Db | 627 | CGGCGCTTTTGAAGAAGACGCGGCTGATCCCTTAAGAATCAACCGAGAGGCTGGAAG | 686 |
| Oy | 829 | GACTTACCTCTGTGTGTCTAGAAATCATGATGTACATCTTGTGTCTTCTCAACCTG | 888 |
| Db | 687 | GACTTACCTCTGTGTGTCTAGAAATCATGATGTACATCTTGTGTCTTCTCAACCTG | 746 |

| | | | |
|----|------|--|------|
| QY | 889 | GGGCGTCGATCGAGATGATATATTTGCTACAGAAAGGCTCAAAAAGCCGAAGGCGACGC | 948 |
| Db | 747 | TGGCTGCTCGATCGAGATGATATATTTGCTACAGAAAGGCTCAAAAAGCCGAAGGCGACGC | 806 |
| QY | 949 | CAAGAAAAACGGCTGTGACTACCTTGCCATCCCATCTGGAACAAGAGAACCTTGCGGTA | 1008 |
| Db | 807 | CAAGAAAAACGGCTGTGACTACCTTGCCATCCCATCTGGAACAAGAGAACCTTGCGGTA | 866 |
| QY | 1009 | CCAGTGGAGGATATGAACAGAGCAGTGTGACATGAGGTGGCCTTGAAACACTGAGGAGCT | 1068 |
| Db | 867 | CCAGTGGAGGATATGAACAGAGCAGTGTGACATGAGGTGGCCTTGAAACACTKGAGGAGCT | 926 |
| QY | 1069 | GGAATCCCATGTTTCAGCAATGTCATATGSCATCGAAGGAGGCCCAAGGGCCCCATATGC | 1128 |
| Db | 927 | GGAATCCCATGTTTCARCAATGTCATATGTCATARGAAGGAGGCCCAAGGGGCCCATATSC | 985 |
| QY | 1129 | TTCCCTTCATGATCCATATGTTGCTGTTTCATTCATTCATCCATACATCAACCTGCGCTGTA | 1188 |
| Db | 986 | TTCCCTTCATGATCATATGTTTGTTCATTAATTAACMAAATACATCKCTTATAGGTTT | 1045 |
| QY | 1189 | GCTTTCACCTGTGACTC 1205 | |
| Db | 1046 | ACTTGTGATCTTAATTC 1062 | |

| | |
|--------------|--|
| RESULT 4 | |
| BX445002 | |
| LOCUS | BK445002 |
| DEFINITION | BK445002 Homo sapiens FETAL BRAIN Hom sapiens cDNA clone |
| CSD0F023YA09 | 5-PRIME, mRNA sequence. |
| | 975 bp mRNA linear EST 04-MAY-2004 |

| | |
|-----------|---|
| ACCESSION | BX445002 |
| VERSION | BX445002.2 |
| KEYWORDS | GI:47009181 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Homo sapiens |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| JOURNAL | 1. (bases 1 to 975) |
| COMMENT | Li, W.B., Gruber, C., Jesssee, J., and Polayes, D. |
| | Full-length cDNA libraries and normalization |
| | Unpublished (2001) |
| | On May 15, 2003 this sequence version replaced gi:30782286. |

Contact: Genoscope
Genoscope - Centre National de Séquençage
2 rue Gaston Cremlieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 6147. r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/5=CS1AF006Z5E05QPl&c=6147.r>.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .975 |

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dr) primer. Five prime
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

| ORIGIN | |
|-----------------------|--------------------------------------|
| Query Match | 51.8% Score 652.6; DB 5; Length 975; |
| Best Local Similarity | 97.5% Pred. No. 2.1e-158; |

| | Matches | 666; | Conservative | 6; | Mismatches | 10; | Indels | 1; | Gaps | 1; |
|----|---------|---------------------------|---|---|------------|-----|--------|----|------|----|
| QY | 349 | AGCCTTGGAAAGCCGCCAGCC | AGCC | CCAGAAAGATGCTCTGCTTCAATAGATTTGTTCCCTTGACT | 408 | | | | | |
| Db | 208 | AGCCTTGGAAAGCCGCCAGCC | AGCC | CCAGAAAGATGCTCTGCTTCAATAGATTTGTTCCCTTGACT | 267 | | | | | |
| QY | 409 | TTCTCTGTCGTTATCTA | CTGGATGAGTCTGCTCCCTGAGTGTGGAAAGTCCCTCG | 468 | | | | | | |
| Db | 268 | TTCTCTGTCGTTATCTA | CTGGATGAGTCTGCTCCCTGAGTGTGGAAAGTCCCTCG | 327 | | | | | | |
| QY | 469 | GAGACGAGAGCCGTGACGAGGCA | AGCC | ATGAGCTGCGTGCATCTCTGCATGAAGAGA | 528 | | | | | |
| Db | 328 | GAGACGAGAGCCGTGACGAGGCA | AGCC | ATGAGCTGCGTGCATCTCTGCATGAAGAGA | 387 | | | | | |
| QY | 529 | GAGAGGTGAGAGCCACCA | CGGTGTGGAAATGGTTCTACAGGCCGAGGCGTAAAGAT | 588 | | | | | | |
| Db | 388 | GAGAGGTGAGAGCCACCA | CGGTGTGGAAATGGTTCTACAGGCCGAGGCGTAAAGAT | 447 | | | | | | |
| QY | 589 | TTTCTTATTTTACGATATCGGAAT | AGGCAACAGGAGGTGAGAGCCCTTTCAGGGGCGC | 648 | | | | | | |
| Db | 448 | TTTCTTATTTTACGATATCGGAAT | AGGCAACAGGAGGTGAGAGCCCTTTCAGGGGCGC | 507 | | | | | | |
| QY | 649 | CTGCAGTGGAAATGGCAGCAAGAGA | CTTCAGAGACGTGTCCATCACTGTGTCAACGTCACT | 708 | | | | | | |
| Db | 508 | CTGCAGTGGAAATGGCAGCAAGAGA | CTTCAGAGACGTGTCCATCACTGTGTCAACGTCACT | 567 | | | | | | |
| QY | 709 | CTGAAGCACTCTGGCCTCTCA | CACTCGCAATGTGTCCCGGAGTTTGATTTAGGCGCAT | 768 | | | | | | |
| Db | 568 | CTGAAGCACTCTGGCCTCTCTCA | CCARCAAAAGTCCCGGAGTTTGATTTAGGCGCAT | 627 | | | | | | |
| QY | 769 | CGGCGCTTTTGTGAAGACAGACG | CGGCTGTATCCCTTAAGATGCACCGGAGAGGCTGGAGAG | 828 | | | | | | |
| Db | 628 | CGGCGCTTTTGTGAAGACAGACG | CGGCTGTATCCCTTAAGATGCACCGGAGAGGCTGGAGAG | 687 | | | | | | |
| QY | 829 | GACTTCACTCTGTGATCTCAGAAAT | CATGATGTACATCTTGTGTCTTCTCAACCTG | 888 | | | | | | |
| Db | 688 | GACTTCACTCTGTGATCTCAGAAAT | CATGATGTACATCTTGTGTCTTCTCAACCTG | 747 | | | | | | |
| QY | 889 | TGCTGTGCTCATCGAGATGATATAT | TTGCTACAGAAAGGTTCTTAAAGCCGGAAGAGCAGCC | 948 | | | | | | |
| Db | 748 | TGCTGTGCTCATCGAGATGATATAT | TTGCTACAGAAAGGTTCTTAAAGCCGGAAGAGCAGCC | 807 | | | | | | |
| QY | 949 | CAAGAAAAACGGCTTGACTACCTT | GCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTA | 1008 | | | | | | |
| Db | 808 | CAAGAAAAACGGCTTGACTACCTT | GCCATCCCATCTGAGAAACAAGAG-AC | CTGCGGTA | 866 | | | | | |
| QY | 1009 | CCAGTGGAGGAATGAACAGAG | 1091 | | | | | | | |
| Db | 867 | MCAGTGGAGGAATGAAMGAGAG | 889 | | | | | | | |

| RESULT 5 | 648 bp | DNA | linear | GSS 12-DEC-2003 |
|--|--------|-----|--------|-----------------|
| AY419145 | | | | |
| LOCUS | | | | |
| DEFINITION | | | | |
| AY419145 Homo sapiens HCM6793 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence. | | | | |

| | |
|-----------|--|
| ACCESSION | AY1419145 |
| VERSION | AY1419145.1 |
| KEYWORDS | GI:39775105 |
| SOURCE | GS5. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | Homo sapiens |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 648) |
| TITLE | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., zheng,X.H., White,T.J., Sninsky,T.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous |

gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 648)

AUTHORS Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Smirsky, D.J., Adams, M.D. and Cargill, M.

TITLE Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source
1..648
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ORIGIN

Query Match 51.3%; Score 646.4; DB 9; Length 648;
Best Local Similarity 99.8%; Pred. No. 7.8e-157;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 376 ATGCTGCTTCAATAGATTGTTCCCTGCTTCTCTGCTTATCTAGGTCAGT 435
1 ATGCTGCTTCAATAGATTGTTCCCTGCTTCTCTGCTTATCTAGGTCAGT 60

QY 436 GTTCTGCTTCCCTGTGTGTGTGAAGTCCCTCGAGACGAGCCGTGCGAGCCAC 495
61 GTTCTGCTTCCCTGTGTGTGTGAAGTCCCTCGAGACGAGCCGTGCGAGCCAC 120

QY 496 ATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
121 ATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

QY 556 GAATGCTTCTACAGCCCGAGGCGGTAAGATTCTTATTTACAGATTCGGAATG 615
181 GAATGCTTCTACAGCCCGAGGCGGTAAGATTCTTATTTACAGATTCGGAATG 240

QY 616 CACGAGAGGTGAGAGACCCCTTTCAGAGGCGCTGAGTGAATGGCAGCAAGAC 675
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QY 676 CAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
301 CAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 736 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
361 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 796 ATCCCTTAAAGATCACCGAGAGGCTGAGAGGACTTCACTCTGTGTCTCAAAA 855
421 ATCCCTTAAAGATCACCGAGAGGCTGAGAGGACTTCACTCTGTGTCTCAAAA 480

QY 856 ATGATGATACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
481 ATGATGATACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 916 TACAGAAAGGTCTCAAAAAGCCGAAAGAGGAGCCCAAGAAAACCGTCTGACT 975
541 TACAGAAAGGTCTCAAAAAGCCGAAAGAGGAGCCCAAGAAAACCGTCTGACT 600

QY 976 ATCCCATCTGAGAAACAAGAACTCTGCGGTACCACTGAGGAATG 1023
601 ATCCCATCTGAGAAACAAGAACTCTGCGGTACCACTGAGGAATG 648

RESULT 5
BP202832 582 bp mRNA linear EST 14-SEP-2004
LOCUS BP202832 Sugano cDNA library, amygdala Homo sapiens cDNA clone
DEFINITION AMR09622, mRNA sequence.
ACCESSION BP202832

VERSION BP202832.1 GI:52054220

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 582)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, O., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

COMMENT Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yuraka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..582
/organism="Homo sapiens"
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ORIGIN

Query Match 45.5%; Score 574; DB 5; Length 582;
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Matches 577; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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61 TGGGAGAGTCCAGTGGGGGTGCTTAAAGGCCCAAGCCCGGCTCCAAAAGCTCCC 120

QY 215 AGGGCTTCCCAAGGACCGGTGCTGCGCCCTTCTGCTGCTGCTGCTGCTGCTG 274
121 AGGGCTTCCCAAGGACCGGTGCTGCGCCCTTCTGCTGCTGCTGCTGCTGCTG 180

QY 275 GCAGTTCCTCCCAAGAGGTTTCTCGAAGAACTCTGAGAGGCGAGTCTTGA 334
181 GCAGTTCCTCCCAAGAGGTTTCTCGAAGAACTCTGAGAGGCGAGTCTTGA 240

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QY 455 TGGAAATGCTTGGAGAGGAGGCGGTGCAAGGCAACCCCATGAAGCTGCTG 514
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QY 635 CTTTCAAGGGGCGCTGCAAGTGAATGCAAGCAAGACCTGCG 676
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 VERSION BP200910.1 GI:52050356
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 582)
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 JOURNAL Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
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 Matches 580; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 RESULT 8 1359 bp mRNA linear HTC 03-APR-2004
 LOCUS AK076466
 DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 library, clone:483314B02 product:VOLTAGE-GATED SODIUM CHANNEL
 BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus
 norvegicus], full insert sequence.
 ACCESSION AK076466
 VERSION AK076466.1 GI:26345409
 KEYWORDS HTC, CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL 99279253
 MEDLINE 10349636
 PUBMED
 REFERENCE 2
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL 20499374
 MEDLINE 11042159
 PUBMED
 REFERENCE 3
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Kono,H., Akiyama,J., Nishi,K., Kitsuana,T., Teshiro,H., Itoh,M.,
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 Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubara,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL 20530913
 MEDLINE 11076861
 PUBMED
 REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 JOURNAL 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL 6 (bases 1 to 1359)
 REFERENCE
 Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
 Hiraoaka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
 Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kono,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
 Tejima,Y., Toyota,T., Yamamura,T., Yamanaka,I., Yasunishi,A.,
 Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (16-APR-2002) Yoshida Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokokoma Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

Source

Bouice

CDS

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ORIGIN

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| | |
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| DEFINITION | Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:CS30046812 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog (Rattus norvegicus), full insert sequence. |
| ACCESSION | AK049747 |
| VERSION | AK049747.1 GI:26334075 |
| KEYWORDS | HTC; CAP TRAPPER. |
| SOURCE | Mus musculus (house mouse) |
| ORGANISM | Mus musculus |

REFERENCE

1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. *Meth. Enzymol.* 303, 19-44 (1999)

AUTHORS Carninci, P., Shibata, Y., Hayashita, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carminci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumaki, T., Tashiro, H., Itoh, M., Saito, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaue, S., Ikegami, T., Kasahigashi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, K., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kir, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)

| REFERENCE | AUTHORS | TITLE | JOURNAL | REFERENCE |
|-----------|--|--|---------|-----------|
| 5 | | The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. | | |
| | | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs | | |
| | | Nature 420, 563-573 (2002) | | |
| | | (bases 1 to 3549) | | |
| | Adachi, S., Aizawa, K., Akinura, T., Arawaka, T., Bono, H., Carninci, P., Futuhata, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., | | | |

Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kankawa, T.,
Kato, H., Kawai, J., Kojima, S., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ono, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muraetsu, M., and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/
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Location/Qualifiers

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Best Local Similarity 88.2%; Pred. No. 1.1e-129;
Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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Query Match 43.0%; Score 542.6; DB 3; Length 3549;
Best Local Similarity 88.2%; Pred. No. 1.1e-129;
Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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Best Local Similarity 88.2%; Pred. No. 1.1e-129;
Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

ORIGIN
Query Match 42.6%; Score 536.6; DB 9; Length 648;
Best Local Similarity 88.2%; Pred. No. 1.1e-129;
Matches 590; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Best Local Similarity 89.3%; Pred. No. 2,8e-128;
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RESULT 11
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LOCUS DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone: C330019103 product: VOLTAGE-GATED SODIUM CHANNEL BETA-3
SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog (Rattus
norvegicus), full insert sequence.
ACCESSION AK049286
VERSION AK049286.1 GI:26093400
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Ariyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, S.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumoto, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4149)
PUBMED 12042159
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imoto, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koyama, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnishi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Yamamoto, M., and Hayashizaki, Y.
TITLE Direct Submission
COMMENT Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. 4149
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C330019103"
/db_xref="taxon:10090"
/clone="C330019103"
/cell_type="ES cells"
/note="VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM
CHANNEL BETA 3 SUBUNIT) homolog (Rattus norvegicus)
(SPTRIQ9K00, evidence: FASTA, 99.5%ID, 100%length,
match=646)
putative"
misc_feature
polya_signal
4129..4134

polyA_site 4149 /note="putative"
 ORIGIN /note="putative"

Query Match 42.2%; Score 531.6; DB 3; Length 4149;
 Best Local Similarity 88.1%; Pred. No. 8,4e-127;
 Matches 590; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

356 GAAGCCGACGAGCCGAGAGAGGCTTCCATGATGTTTCCCGGCTTCTCG 415
 390 GAACCCACTTACGAGAGAGAGGCTTCCATGATGTTTCCCGGCTTCTCG 449
 416 TCCCTATCTACTGAGGCTGCTGCTTCCGCTTCCGCTTCCGCTTCCG 474
 450 TCCCTATCTACTGAGGCTGCTGCTTCCGCTTCCGCTTCCGCTTCCG 509
 475 GAGCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
 510 GAAGCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 569
 535 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
 570 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 629
 595 ATTTACGAGTATCGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654
 630 ATTTACGAGTATCGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
 655 TGGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
 690 TGGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 749
 715 GACTCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 774
 750 GACTCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 809
 775 TTTTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 834
 810 TTTTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 869
 835 ACCCTGCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTG 894
 870 ACCCTGCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTG 929
 895 CTCATCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
 930 TTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
 955 AACGCTGCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTG 1014
 990 AATGCTGCTGCTCTACACCTGCAATGCTGCTGCTGCTGCTGCTGCTG 1049

RESULT 12
 BB614118 672 bp mRNA linear EST 26-OCT-2001
 LOCUS BB614118 RIKEN full-length enriched, 0 day neonate head Mus
 DEFINITION musculus cDNA clone 4833414B02 5', mRNA sequence.

ACCESSION BB614118
 VERSION BB614118.1 GI:16454578
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 672)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,

TITLE JOURNAL
 COMMENT

Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shikata,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
 Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y., and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamakawa,I.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., and
 Hayashizaki,Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

FEATURES

source

Location/Qualifiers
 1..672
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4833414B02"
 /sex="mixed"
 /tissue_type="head"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /clone_1ib="RIKEN full-length enriched, 0 day neonate
 head"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'-
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rct = 10.0 and subtraction to Rct = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5'-GAGAGAGAGATCTCGAGTTATTAATTAATTCCTCCCTCCCTCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda PflC I."

ORIGIN

Query Match

41.6%; Score 524.4; DB 2; Length 672;

Best Local Similarity 87.0%; Pred. No. 4.2e-125;
Matches 576; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 332 AGGGAATCTCTCTGTAGCTTGAAGAGCCGACGAGGAGAGGCTGCTCAATA 391
DB 11 AGGAATCTCTCTGTAGCTTGAAGAGCCGACGAGGAGAGGCTGCTCAATA 70
QY 392 GATTTGTTCCCTGAGCTTCTGTGCTTATCTAGTGGTCAAGTGTGCTTCCCTGT 451
DB 71 GATTTGTTCCCTGAGCTTCTGTGCTTATCTAGTGGTCAAGTGTGCTTCCCTGT 130
QY 452 GTGTGAGAGTCCCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511
DB 131 GTGTGAGAGTCCCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 190
QY 512 TCTCTGCTGAG 571
DB 191 TCTCTGCTGAG 250
QY 572 CCGAGGAGGAGTAAAGATTCTTATTAGAGATGAGATGAGATGAGATGAGATG 631
DB 251 CCGAGGAGGAGTAAAGATTCTTATTAGAGATGAGATGAGATGAGATGAGATG 310
QY 632 GCCCTTTGAG 691
DB 311 GCCCTTTGAG 370
QY 692 CTGTGCTGAG 751
DB 371 CTGTGCTGAG 430
QY 752 TTGAGTTGAG 811
DB 431 TTGAGTTGAG 490
QY 812 CCGAGAGAGGAG 871
DB 491 CCGAGAGAGGAG 550
QY 872 TGGTCTTCTGAG 931
DB 551 TGGTCTTCTGAG 610
QY 932 AAGCCGAAG 991
DB 611 AAGCCGAAG 670
QY 992 AG 993
DB 671 AG 672

RESULT 13
BM933157 636 bp mRNA linear EST 13-MAR-2002
LOCUS UI-M-BH3-bag-d-04-0-UI-r1 NIH_BMAP_M_S4 Mus musculus cDNA clone
DERIVATION UI-M-BH3-bag-d-04-0-UI-S, mRNA sequence.
ACCESSION BM933157
VERSION BM933157.1 GI:19392309
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 636)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 57044477
PUBMED 8889548
COMMENT Contact: Chin, H
National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9690
Email: mestr@mail.nih.gov
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
Location/Qualifiers
1. 636
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-bag-d-04-0-UI"
/dev stage="27-32 days"
/lab host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="vector: pTV3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, ganglionic bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 41.3%; Score 521.4; DB 5; Length 636;
Best Local Similarity 88.8%; Pred. No. 2.5e-124;
Matches 564; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 371 AGAAGATGCTGCTCAATAGATTGTTCCCTGAGCTTCTCGTATTACTATGAG 430
DB 2 AAAAGATGCTGCTCAATAGATTGTTCCCTGAGCTTCTCGTATTACTATGAG 61
QY 431 TCAGTGTGCTTCCCTGAGCTTCTCGTATTACTATGAGTGTGAGAGAGAGAG 490
DB 62 TCAGTGTGCTTCCCTGAGCTTCTCGTATTACTATGAGTGTGAGAGAGAGAG 121
QY 491 ACCCATGAAGCTGCTGATCTCTGATGAAGAGAGAGAGAGAGAGAGAGAGAG 550
DB 122 ATTCATGAAGCTGATCTCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 551 TGGTGAAGTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
DB 182 TGGTGAAGTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
QY 611 ATGGCCACAG 670
DB 242 ATGGCCACAG 301

671 ACCTGACAGAGCTGTCTCATCTGTCTCAACGTCATCTGTGACGACTCTGGCCCTCTACA 730
DB ACCTGACAGAGCTGTCTCATCTGTCTCAACGTCATCTGTGACGACTCTGGCCCTCTACA 361
671 CCTGCAATGTGTCCCGGAGTTTGAAGTTTGAAGCCCATCGCCCTTTGTGAAGACGACGC 790
DB CATGTAATGTGTCCCGGAGTTTGAAGTTTGAAGCCCATCGCCCTTTGTGAAGACGACCA 421
791 GAGCGATCCCCCTTAAGAGTACCCGAGAGGCTGAGAGGACTTCACTCTGTGTGTCTGAG 850
DB GACTATATCCCTTGAGTCACTGTAAGAGGCGGAGAGGACTTCACTCTGTGTGTCTGAG 481
422 GACTATATCCCTTGAGTCACTGTAAGAGGCGGAGAGGACTTCACTCTGTGTGTCTGAG 910
DB AAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
482 AAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 911
DB ATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCG 970
542 ATTGCTACAGAAAGGTCTCAAAAGGTCTCAAAAGGTCTCAAAAGGTCTCAAAAGGTCT 601
DB TTGCGATCCCATCTGAGAAAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
971 TTGCGATCCCATCTGAGAAAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602
TTGCGATCCCATCTGAGAAAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636

RESULT 14
BC058083 4105 bp mRNA linear HTC 19-NOV-2003
LOCUS Mus musculus sodium channel, voltage-gated, type III, beta, mRNA
DEFINITION (cDNA clone IMAGE:6826414), containing frame-shift errors.
ACCESSION BC058083
VERSION BC058083.1 GI:34784518
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4105)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheeler, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheer, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Iqbal, N.A., Peters, G.J.,
Abrahamson, R.D., Millar, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huijyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettleman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalka, U., Smalins, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED 22388257
12477932
2 (bases 1 to 4105)
REFERENCE Strausberg, R.
AUTHORS Direct Submission
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgs.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chin, Chris Ewell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Mess, Pawan Pandoh, Anna-Lies Prabh, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 126 Row: 1 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23943798
This clone has the following problem: frame shifted.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6826414"
/issue_type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc"
/clone_lib="NIH BMAP_FY0"
/lab_host="DH10B"
/note="Vector: pYX-ASC"

ORIGIN
Query Match 40.8%; Score 514.2; DB 3; Length 4105;
Best Local Similarity 87.6%; Pred. No. 2.8e-132;
Matches 586; Conservative 0; Mismatches 78; Indels 5; Gaps 2;

356 GAAACCCGACAGCCAGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 415
DB GAAACCCGACAGCCAGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 395
336 GAAACCCGACAGCCAGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 415
DB GAAACCCGACAGCCAGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 395
416 TGTCTATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
DB TGTCTATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451
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452 AGGCGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 535
DB AGGCGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 511
536 TGAAGGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 595
DB TGAAGGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 571
512 TGAAGGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 595
DB TGAAGGCGACAGGAGCAAGCCATGAGAGTGCCTGCTCAATAGTGTTCCTCCCTGCTCTCTCG 571
596 TTTACGAGTATGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
DB TTTACGAGTATGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
572 TATATGATATGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
DB TATATGATATGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
656 GGAATGCGAGCAAGAGCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
DB GGAATGCGAGCAAGAGCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690
632 GGAATGCGAGCAAGAGCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
DB GGAATGCGAGCAAGAGCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690
716 ACTCTGCGCTTACAGCTGCAATGATGCTCCGAGAGTTTGAAGTTTGAAGCGGAGCGGCTT 775
DB ACTCTGCGCTTACAGCTGCAATGATGCTCCGAGAGTTTGAAGTTTGAAGCGGAGCGGCTT 750
691 ACTCTGCGCTTACAGCTGCAATGATGCTCCGAGAGTTTGAAGTTTGAAGCGGAGCGGCTT 775
DB ACTCTGCGCTTACAGCTGCAATGATGCTCCGAGAGTTTGAAGTTTGAAGCGGAGCGGCTT 750
776 TTGTGAAGAGAGCGGCTGATCCCTTGAAGAGTACCGAGAGGCTGAGAGAGGAGGAGGAGGAG 835
DB TTGTGAAGAGAGCGGCTGATCCCTTGAAGAGTACCGAGAGGCTGAGAGAGGAGGAGGAGGAG 810
751 TTGTGAAGAGAGCGGCTGATCCCTTGAAGAGTACCGAGAGGCTGAGAGAGGAGGAGGAGGAG 835
DB TTGTGAAGAGAGCGGCTGATCCCTTGAAGAGTACCGAGAGGCTGAGAGAGGAGGAGGAGGAG 810
836 CCTCTGAGTCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
DB CCTCTGAGTCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
811 CCTCTGAGTCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
DB CCTCTGAGTCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
896 TCATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
DB TCATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

Db 871 TTATGAGATGATATGCTACGAGAAAGCTCTTAAGCCGGAAGAGCGCTCAGAAA 930
 Qy 956 ACCGCTGACCTACCTTCCATCCATCTGAGAAAGAACTTCCGCGTACCACTGG 1015
 Db 931 ATCCGTGACTACCTTCTATCCCTTCAGAGAAAGAACTCTGTGTGATCCCTGG 990
 Qy 1016 AGGAATAGA 1024
 Db 991 AGGAATAGA 999

RESULT 15
 AL534136 1078 bp mRNA linear EST 24-MAR-2004
 LOCUS CS0DF005Y102 5-PRIME, mRNA sequence.
 DEFINITION AL534136 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 AL534136
 ACCESSION AL534136
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1078)
 Lj.W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:30539643.
 COMMENT
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

This sequence belongs to sequence cluster 6147.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0DF005B010P1ac=6147.r.
 location/Qualifiers

FEATURES

source

1..1078
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="CS0DF005Y102"
 /issue_type="FETAL BRAIN"
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 /note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo (dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 40.7%; Score 513; DB 1; Length 1078;
 Best Local Similarity 91.5%; Pred. No. 4.3e-122;
 Matches 589; Conservative 9; Mismatches 35; Indels 11; Gaps 5;
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 Db 392 CTCCTTCGAGCTGAGCTTACCTCGGCGCAACGAGCGAGGCGCGAGTGGAA 451
 Qy 63 GCTGAGTTCCGGGCTGAGCGGAGGCGAGCTGCTGCTGAGCGCGGCGAGAGC 122
 Db 452 GCTGAGTTCCGGGCTGAGCGGAGGCGAGCTGCTGCTGAGCGCGGCGAGAGC 511
 Qy 123 GGGCGGAGAGCGGCTGAGCTGCTGCGAATGGGAGGTCAGTGGGCTGCTTAAGG 182
 Db 512 GGGCGGAGAGCGGCTGAGCTGCTGCGAATGGGAGGTCAGTGGGCTGCTTAAGG 569

Qy 183 CCCAAAGCCCCACCCCGCTCAAAAAGCTCCAGAGGCTCCCGACCGGCTGCTGCG 242
 Db 570 CCCAAAGCCCCACCCCGCTCAAAAAGCTCCAGAGGCTCCCGACCGGCTGCTGCG 629
 Qy 243 CCTTCTCGGTGAGAAAGTGGCCCCCTGGGGGCACTTCTCCAAAGGTTTCTTGA 302
 Db 630 CTTTCTCGGTGAGAAAGTGGCCCCCTGGGGGCACTTCTCCAAAGGTTTCTTGA 689
 Qy 303 AGAATCTGAGAGGGCGGAGTCTTGAACCGAGGAAATCTCTGTGTAGCTTGAAGCCG 362
 Db 690 AGAATCTGAGAGGGCGGAGTCTTGAACCGAGGAAATCTCTGTGTAGCTTGAAGCCG 748
 Qy 363 CCAGCCCCAGAAAGTGGCTCTTCAATAGATTGTTCCCTGAGCTTCTGNGCTTAT 422
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 Db 869 GCAAGGCAACCCCATGAAGCTGCGCTGCATCTCTGATGAAGAGAGAGTGAAGC 928
 Qy 543 CACCACGGTGGTGAATGTTCTACAGGCGCGAGGCGGTAAAGATTCTTATTACGA 602
 Db 929 CACCACGGTGGTGAATGTTCTACAGGCGCGAGGCGGTAAAGATTCTTATTACGA 983
 Qy 603 GATTCGAATGAGCCACGAGAGGTGAGAGCCCTTTCAGGGGC 646
 Db 984 GATTCGAATGAGCCACGAGAGGTGAGAGCCCTTTCAGGGGC 1024

Search completed: April 1, 2005, 21:54:09
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